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(54) Title: REGULATION OF HUMAN LYSOSOMAL ACID LIPASE

(57) Abstract: Reagents which regulate human lysosomal acid lipase and reagents which bind to human lysosomal acid lipase gene products can play a role in preventing, ameliorating, or correcting dysfunctions or diseases including, but not limited to, cancer, CNS disorders, obesity, COPD, diabetes, and cardiovascular disorders.

WO 02/36754 A2

## REGULATION OF HUMAN LYSOSOMAL ACID LIPASE

5 This application incorporates by reference Serial No. 60/244,215 filed October 31, 2000, and Serial No. 60/251,401 filed December 6, 2001.

## TECHNICAL FIELD OF THE INVENTION

10 The invention relates to the area of lipase enzymes. More particularly, the invention relates to the identification of human lysosomal acid lipase and its regulation.

## BACKGROUND OF THE INVENTION

15 Adipose tissues are repositories of energy in the form of complex, insoluble lipoproteins. The movement of this potential energy into energy-requiring cells involves the hydrolysis of the lipoprotein by lipases. In general, triglycerides are the substrate of lipases. The reaction produces lower molecular weight fatty acids and  $\beta$ -mono- and diglycerides. The resultant lipids are absorbed into digestive tract cells with the aid of emulsifying bile acids. The triglycerides are re-synthesized in the  
20 endoplasmic reticulum as chylomicrons. See review by Pullinger and Kane, "Lipid Metabolism and Transport," in MOLECULAR BIOLOGY AND BIOTECHNOLOGY, Meyers, ed., VCH Publishers, New York, 1995. The chylomicrons are transported by the lymph system away from the site of absorption.

25 Various tissues (*e.g.* skeletal muscle and heart) synthesize a lipase enzyme, lipoprotein lipase (PLP). The enzyme is secreted by parenchymal cells and attaches to the endothelial surface as a homodimer. PLP acts on the triglyceride core of the chylomicrons. The fatty acids released by LDL are taken up by neighboring tissue cells and used as energy or stored as triglycerides. *Id.* Epinephrine and protein  
30 kinase induce the lipase activity.

The pancreas is the source of another lipase, pancreatic lipase, which constitutes as much as 2.5% of the pancreatic juice. Faustinella *et al.*, *J. Biol. Chem.* 266, 9481-85, 1991. Hepatic lipases are also known. Cai *et al.*, *Biochemistry* 23, 8966-71, 1989.

5 Lipoprotein, hepatic, and pancreatic lipases are members of a family of enzymes and share extensive structural motifs generally believed important in their intracellular localization and function. These sites include a lipid-binding domain, a Ser-centered consensus active-site motif, Gly-Xaa-Ser-Xaa-Gly (at position 132 in human lipoprotein lipase), and a conserved Ser-His dipeptide found in the amino-terminal  
10 domain of most lipases. Persson *et al.*, *Eur. J. Biochem.* 17, 39-45, 1989; Cai, *et al.*, *supra*; Ameis *et al.*, *J. Biol. Chem.* 12, 6552-55, 1990; Kirchgessner *et al.*, *Proc. Natl. Acad. Sci.* 89, 9647-51, 1989; Feller *et al.*, *DNA Cell Biol.* 10, 381-88, 1991; Faustinella *et al.*, *supra*; Sims *et al.*, *Gene* 131, 281-85, 1993; and Derewenda & Cambillau, *J. Biol. Chem.* 266, 23112-19, 1991. A good assay for lipases in general  
15 and lipoprotein lipase in particular is based on hydrolysis of water soluble *p*-nitrophenylbutarate. Shirai and Jackson, *J. Biol. Chem.* 257, 1253-58, 1982.

Reduced levels of active pancreatic lipase characterize a number of lipid malabsorption illnesses. About 80% of cystic fibrosis patients develop pancreatic  
20 lipase deficiency shortly after birth. Alcoholics suffer from pancreatitis, a condition where the pancreas is impaired and fats are malabsorbed, resulting in malnutrition. Fetuses have low pancreatic lipase activity, but a high carbohydrate diet. After birth, the milk diet is suddenly high in fat and steatorrhea (fat molecules in feces), usually temporary, occurs, with an accompanying loss of energy. The present treatment of  
25 low pancreatic lipase activity in all conditions is inadequate, consisting of large doses of crude pig pancreas enzyme preparations. The low pH of the gut destroys the enzyme. The large doses thus necessary are difficult to administer. U.S. Patent 5,858,755.

30 Obviously, heart disease and heart attacks are correlated with fatty acids levels. Wolman disease and cholesteryl ester storage disease are characterized by a

deficiency in activity of lysosomal acid lipase and result in massive accumulation of cholesteryl esters and triglycerides in most tissues of the body. U.S. Patent 6,066,653.

- 5 Other uses for lipases are well established. For example, lipolytic enzymes have been used in detergents to remove lipid or fatty stains from clothes and other textiles. U.S. Patent 5,892,013.

- 10 Given the great importance of lipases in metabolism, metabolic disease, and cholesterol control, a need exists for identification of novel lipase genes which can be regulated and provide therapeutic options.

#### **SUMMARY OF THE INVENTION**

- 15 It is an object of the invention to provide reagents and methods of regulating a human lysosomal acid lipase. This and other objects of the invention are provided by one or more of the embodiments described below.

- 20 One embodiment of the invention is a lysosomal acid lipase polypeptide comprising an amino acid sequence selected from the group consisting of:  
amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 2;  
the amino acid sequence shown in SEQ ID NO: 2;  
amino acid sequences which are at least about 54% identical to the amino acid  
25 sequence shown in SEQ ID NO: 5;  
the amino acid sequence shown in SEQ ID NO: 5;  
amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 6; and  
the amino acid sequence shown in SEQ ID NO: 6.

- 4 -

Yet another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a lysosomal acid lipase polypeptide comprising an amino acid sequence selected from the group consisting of:

- 5 amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 2;
  - the amino acid sequence shown in SEQ ID NO: 2;
  - amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 5;
  - 10 the amino acid sequence shown in SEQ ID NO: 5;
  - amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 6; and
  - the amino acid sequence shown in SEQ ID NO: 6.
- 15 Binding between the test compound and the lysosomal acid lipase polypeptide is detected. A test compound which binds to the lysosomal acid lipase polypeptide is thereby identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the activity of the lysosomal acid lipase.
- 20 Another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a polynucleotide encoding a lysosomal acid lipase polypeptide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:
- 25 nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;
  - the nucleotide sequence shown in SEQ ID NO: 1;
  - nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 4;
  - 30 the nucleotide sequence shown in SEQ ID NO: 4;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 7; and  
the nucleotide sequence shown in SEQ ID NO:7.

- 5 Binding of the test compound to the polynucleotide is detected. A test compound which binds to the polynucleotide is identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the amount of the lysosomal acid lipase through interacting with the lysosomal acid lipase mRNA.
- 10 Another embodiment of the invention is a method of screening for agents which regulate extracellular matrix degradation. A test compound is contacted with a lysosomal acid lipase polypeptide comprising an amino acid sequence selected from the group consisting of:
- 15 amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 2;  
the amino acid sequence shown in SEQ ID NO: 2;  
amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 5;  
the amino acid sequence shown in SEQ ID NO:5;
- 20 amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 6; and  
the amino acid sequence shown in SEQ ID NO: 6.

- 25 A lysosomal acid lipase activity of the polypeptide is detected. A test compound which increases lysosomal acid lipase activity of the polypeptide relative to lysosomal acid lipase activity in the absence of the test compound is thereby identified as a potential agent for increasing extracellular matrix degradation. A test compound which decreases lysosomal acid lipase activity of the polypeptide relative to lysosomal acid lipase activity in the absence of the test compound is thereby
- 30 identified as a potential agent for decreasing extracellular matrix degradation.

Even another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a lysosomal acid lipase product of a polynucleotide which comprises a nucleotide sequence selected from the group consisting of:

- 5 nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;  
the nucleotide sequence shown in SEQ ID NO: 1;  
nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 4;  
10 the nucleotide sequence shown in SEQ ID NO: 4;  
nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 7; and  
the nucleotide sequence shown in SEQ ID NO: 7.
- 15 Binding of the test compound to the lysosomal acid lipase product is detected. A test compound which binds to the lysosomal acid lipase product is thereby identified as a potential agent for decreasing extracellular matrix degradation.

- 20 Still another embodiment of the invention is a method of reducing extracellular matrix degradation. A cell is contacted with a reagent which specifically binds to a polynucleotide encoding a lysosomal acid lipase polypeptide or the product encoded by the polynucleotide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:
- 25 nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;  
the nucleotide sequence shown in SEQ ID NO: 1;  
nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 4;  
the nucleotide sequence shown in SEQ ID NO: 4;  
30 nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 7; and

the nucleotide sequence shown in SEQ ID NO:7.

Lysosomal acid lipase activity in the cell is thereby decreased.

5 The invention thus provides a human lysosomal acid lipase which can be used to identify test compounds which may act, for example, as activators or inhibitors at the enzyme's active site. Human lysosomal acid lipase and fragments thereof also are useful in raising specific antibodies which can block the enzyme and effectively reduce its activity.

10

#### **BRIEF DESCRIPTION OF THE DRAWINGS**

Fig. 1 shows the DNA-sequence encoding a lysosomal acid lipase Polypeptide (SEQ ID NO :1).

15 Fig. 2 shows the amino acid sequence deduced from the DNA-sequence of Fig.1 (SEQ ID NO:2).

Fig. 3 shows the amino acid sequence of the protein identified by SwissProt Accession No. P38571 (SEQ ID NO:3).

20 Fig. 4 shows the DNA-sequence encoding a lysosomal acid lipase Polypeptide (SEQ ID NO:4).

Fig. 5 shows the amino acid sequence deduced from the DNA-sequence of Fig. 4 (SEQ ID NO:5).

Fig. 6 shows the amino acid sequence of a lysosomal acid lipase Polypeptide (SEQ ID NO:6).

25 Fig. 7 shows the DNA-sequence encoding a lysosomal acid lipase Polypeptide (SEQ ID NO:7).

Fig. 8 shows the BLASTP alignment of human lysosomal acid lipase (SEQ ID NO:2) with the protein identified with SwissProt Accession No. P38571 (SEQ ID NO:3).

30 Fig. 9 shows the BLASTP - alignment of 135\_PROTEIN (SEQ ID NO:2) against pdb|1HLG|1HLG-A.



Fig. 10 shows the BLASTP alignment of 135\_v2\_TR1 (SEQ ID NO:2) against swiss[P38571]LICH\_HUMAN.

Fig. 11 shows the BLASTP - alignment of 135\_v2\_TR1 (SEQ ID NO:2) against pdb[1HLG]1HLG-A lipase, gastric.

5 Fig. 12 shows the Intron-Exon borders.

Fig. 13 shows the Genewise output feature table.

### DETAILED DESCRIPTION OF THE INVENTION

10 The invention relates to an isolated polynucleotide encoding a lysosomal acid lipase polypeptide and being selected from the group consisting of:

- a) a polynucleotide encoding a lysosomal acid lipase polypeptide comprising an amino acid sequence selected from the group consisting of:
- 15 amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 2;  
the amino acid sequence shown in SEQ ID NO: 2;  
amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 5;  
20 the amino acid sequence shown in SEQ ID NO:5;  
amino acid sequences which are at least about 54% identical to the amino acid sequence shown in SEQ ID NO: 6; and  
the amino acid sequence shown in SEQ ID NO: 6.
- 25 b) a polynucleotide comprising the sequence of SEQ ID NO: 1, 4 or 7;
- c) a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b);

- 9 -

- d) a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code; and
- 5 e) a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d).

Furthermore, it has been discovered by the present applicant that a novel lysosomal acid lipase, particularly a human lysosomal acid lipase, is a discovery of the present invention. Human lysosomal acid lipase comprises an amino acid sequence shown in  
10 SEQ ID NO:2, 5, or 6. Coding sequences for human lysosomal acid lipase are shown in SEQ ID NOS:1, 4, and 7. This sequence is located on chromosome 10.

Human lysosomal acid lipase is 53% identical over 92 amino acids to the human protein identified with SwissProt Accession No. P38571 and annotated as  
15 "LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13)" (Fig. 8). Human lysosomal acid lipase also is 50% identical over 89 amino acids to 136\_PROTEIN (SEQ ID NO:2) against pfam|hmm|abhydrolase (Fig. 9); 53% over 396 amino acids to  
20 swiss|P38571|LICH\_HUMAN (Fig. 10); and 52% identical over 366 amino acids to pdb|1HLG|1HLG-A lipase, gastric (Fig. 11).

Human lysosomal acid lipase of the invention is expected to be useful for the same purposes as previously identified lysosomal acid lipase enzymes. Human lysosomal  
25 acid lipase is believed to be useful in therapeutic methods to treat disorders such as cancer, CNS disorders, obesity, COPD, diabetes, and cardiovascular disorders. Human lysosomal acid lipase also can be used to screen for human lysosomal acid lipase activators and inhibitors.

### Polypeptides

Human lysosomal acid lipase polypeptides according to the invention comprise at least 6, 10, 15, 20, 25, 50, 75, or 93 contiguous amino acids selected from the amino acid sequence shown in SEQ ID NO:2, 5, or 6 or a biologically active variant thereof, as defined below. A lysosomal acid lipase polypeptide of the invention therefore can be a portion of a lysosomal acid lipase protein, a full-length lysosomal acid lipase protein, or a fusion protein comprising all or a portion of a lysosomal acid lipase protein.

### Biologically Active Variants

Human lysosomal acid lipase polypeptide variants which are biologically active, e.g., retain a lipase activity, also are lysosomal acid lipase polypeptides. Preferably, naturally or non-naturally occurring lysosomal acid lipase polypeptide variants have amino acid sequences which are at least about 54, 60, 65, or 70, preferably about 75, 80, 85, 90, 96, 96, or 98% identical to the amino acid sequence shown in SEQ ID NO:2 or a fragment thereof. Percent identity between a putative lysosomal acid lipase polypeptide variant and an amino acid sequence of SEQ ID NO:2, 5, or 6 is determined using the Blast2 alignment program (Blosun62, Expect 10, standard genetic codes).

Variations in percent identity can be due, for example, to amino acid substitutions, insertions, or deletions. Amino acid substitutions are defined as one for one amino acid replacements. They are conservative in nature when the substituted amino acid has similar structural and/or chemical properties. Examples of conservative replacements are substitution of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine.

Amino acid insertions or deletions are changes to or within an amino acid sequence. They typically fall in the range of about 1 to 5 amino acids. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological or immunological activity of a lysosomal acid lipase polypeptide can be

found using computer programs well known in the art, such as DNASTAR software. Whether an amino acid change results in a biologically active lysosomal acid lipase polypeptide can readily be determined by assaying for lipase activity, as is known in the art and described for example, in Example 4, below.

5

### Fusion Proteins

Fusion proteins are useful for generating antibodies against lysosomal acid lipase polypeptide amino acid sequences and for use in various assay systems. For example, fusion proteins can be used to identify proteins which interact with portions of a lysosomal acid lipase polypeptide. Protein affinity chromatography or library-based assays for protein-protein interactions, such as the yeast two-hybrid or phage display systems, can be used for this purpose. Such methods are well known in the art and also can be used as drug screens.

10

A lysosomal acid lipase polypeptide fusion protein comprises two polypeptide segments fused together by means of a peptide bond. The first polypeptide segment comprises at least 6, 10, 15, 20, 25, 50, 75, or 93 contiguous amino acids of SEQ ID NO:2, 5, or 6 or of a biologically active variant, such as those described above. The first polypeptide segment also can comprise full-length lysosomal acid lipase protein.

15  
20

The second polypeptide segment can be a full-length protein or a protein fragment. Proteins commonly used in fusion protein construction include  $\beta$ -galactosidase,  $\beta$ -glucuronidase, green fluorescent protein (GFP), autofluorescent proteins, including blue fluorescent protein (BFP), glutathione-S-transferase (GST), luciferase, horseradish peroxidase (HRP), and chloramphenicol acetyltransferase (CAT). Additionally, epitope tags are used in fusion protein constructions, including histidine (His) tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Other fusion constructions can include maltose binding protein (MBP), S-tag, Lex a DNA binding domain (DBD) fusions, GAL4 DNA binding domain fusions, and herpes simplex virus (HSV) BP16 protein fusions. A fusion protein also can be engineered to contain a cleavage site located between

25

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the lysosomal acid lipase polypeptide-encoding sequence and the heterologous protein sequence, so that the lysosomal acid lipase polypeptide can be cleaved and purified away from the heterologous moiety.

5 A fusion protein can be synthesized chemically, as is known in the art. Preferably, a fusion protein is produced by covalently linking two polypeptide segments or by standard procedures in the art of molecular biology. Recombinant DNA methods can be used to prepare fusion proteins, for example, by making a DNA construct which comprises coding sequences selected from the complement of SEQ ID NO:1,  
10 4, or 7 in proper reading frame with nucleotides encoding the second polypeptide segment and expressing the DNA construct in a host cell, as is known in the art. Many kits for constructing fusion proteins are available from companies such as Promega Corporation (Madison, WI), Stratagene (La Jolla, CA), CLONTECH (Mountain View, CA), Santa Cruz Biotechnology (Santa Cruz, CA), MBL  
15 International Corporation (MIC; Watertown, MA), and Quantum Biotechnologies (Montreal, Canada; 1-888-DNA-KITS).

#### Identification of Species Homologs

Species homologs of human lysosomal acid lipase polypeptide can be obtained using  
20 lysosomal acid lipase polypeptide polynucleotides (described below) to make suitable probes or primers for screening cDNA expression libraries from other species, such as mice, monkeys, or yeast, identifying cDNAs which encode homologs of lysosomal acid lipase polypeptide, and expressing the cDNAs as is known in the art.

25

#### Polynucleotides

A lysosomal acid lipase polynucleotide can be single- or double-stranded and comprises a coding sequence or the complement of a coding sequence for a lysosomal acid lipase polypeptide. Coding sequences for human lysosomal acid  
30 lipase are shown in SEQ ID NOS:1, 4, and 7.

Degenerate nucleotide sequences encoding human lysosomal acid lipase polypeptides, as well as homologous nucleotide sequences which are at least about 50, 55, 60, 65, 70, preferably about 75, 90, 96, or 98% identical to the nucleotide sequence shown in SEQ ID NO:1, or 7 or their complements also are lysosomal acid lipase polynucleotides. Percent sequence identity between the sequences of two polynucleotides is determined using computer programs such as ALIGN which employ the FASTA algorithm, using an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2. Complementary DNA (cDNA) molecules, species homologs, and variants of lysosomal acid lipase polynucleotides which encode biologically active lysosomal acid lipase polypeptides also are lysosomal acid lipase polynucleotides. Polynucleotides comprising at least 6, 7, 8, 9, 10, 12, 15, 18, 20, or 25 contiguous nucleotides of SEQ ID NO:1, 4, or 7 or their complements also are lysosomal acid lipase polynucleotides. Such polynucleotides can be used, for example, as hybridization probes or antisense oligonucleotides.

#### Identification of Polynucleotide Variants and Homologs

Variants and homologs of the lysosomal acid lipase polynucleotides described above also are lysosomal acid lipase polynucleotides. Typically, homologous lysosomal acid lipase polynucleotide sequences can be identified by hybridization of candidate polynucleotides to known lysosomal acid lipase polynucleotides under stringent conditions, as is known in the art. For example, using the following wash conditions—2X SSC (0.3 M NaCl, 0.03 M sodium citrate, pH 7.0), 0.1% SDS, room temperature twice, 30 minutes each; then 2X SSC, 0.1% SDS, 50 °C once, 30 minutes; then 2X SSC, room temperature twice, 10 minutes each—homologous sequences can be identified which contain at most about 25-30% basepair mismatches. More preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches.

Species homologs of the lysosomal acid lipase polynucleotides disclosed herein also can be identified by making suitable probes or primers and screening cDNA expression libraries from other species, such as mice, monkeys, or yeast. Human

variants of lysosomal acid lipase polynucleotides can be identified, for example, by screening human cDNA expression libraries. It is well known that the  $T_m$  of a double-stranded DNA decreases by 1-1.5 °C with every 1% decrease in homology (Bonner *et al.*, *J. Mol. Biol.* 81, 123 (1973). Variants of human lysosomal acid lipase polynucleotides or lysosomal acid lipase polynucleotides of other species can therefore be identified by hybridizing a putative homologous lysosomal acid lipase polynucleotide with a polynucleotide having a nucleotide sequence of SEQ ID NO:1, 4, or 7 or the complement thereof to form a test hybrid. The melting temperature of the test hybrid is compared with the melting temperature of a hybrid comprising polynucleotides having perfectly complementary nucleotide sequences, and the number or percent of basepair mismatches within the test hybrid is calculated.

Nucleotide sequences which hybridize to lysosomal acid lipase polynucleotides or their complements following stringent hybridization and/or wash conditions also are lysosomal acid lipase polynucleotides. Stringent wash conditions are well known and understood in the art and are disclosed, for example, in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2d ed., 1989, at pages 9.50-9.51.

Typically, for stringent hybridization conditions a combination of temperature and salt concentration should be chosen that is approximately 12-20 °C below the calculated  $T_m$  of the hybrid under study. The  $T_m$  of a hybrid between a lysosomal acid lipase polynucleotide having a nucleotide sequence shown in SEQ ID NO:1, 4, or 7 or the complement thereof and a polynucleotide sequence which is at least about 50, preferably about 75, 90, 96, or 98% identical to one of those nucleotide sequences can be calculated, for example, using the equation of Bolton and McCarthy, *Proc. Natl. Acad. Sci. U.S.A.* 48, 1390 (1962):

$$T_m = 81.5\text{ }^{\circ}\text{C} - 16.6(\log_{10}[\text{Na}^+]) + 0.41(\%G + C) - 0.63(\%\text{formamide}) - 600/l,$$

where  $l$  = the length of the hybrid in basepairs.

Stringent wash conditions include, for example, 4X SSC at 65 °C, or 50% formamide, 4X SSC at 42 °C, or 0.5X SSC, 0.1% SDS at 65 °C. Highly stringent wash conditions include, for example, 0.2X SSC at 65 °C.

5     Preparation of Polynucleotides

A lysosomal acid lipase polynucleotide can be isolated free of other cellular components such as membrane components, proteins, and lipids. Polynucleotides can be made by a cell and isolated using standard nucleic acid purification techniques, or synthesized using an amplification technique, such as the polymerase chain reaction (PCR), or by using an automatic synthesizer. Methods for isolating polynucleotides are routine and are known in the art. Any such technique for obtaining a polynucleotide can be used to obtain isolated lysosomal acid lipase polynucleotides. For example, restriction enzymes and probes can be used to isolate polynucleotide fragments which comprises lysosomal acid lipase nucleotide sequences. Isolated polynucleotides are in preparations which are free or at least 70, 80, or 90% free of other molecules.

Human lysosomal acid lipase cDNA molecules can be made with standard molecular biology techniques, using lysosomal acid lipase mRNA as a template. Human lysosomal acid lipase cDNA molecules can thereafter be replicated using molecular biology techniques known in the art and disclosed in manuals such as Sambrook *et al.* (1989). An amplification technique, such as PCR, can be used to obtain additional copies of polynucleotides of the invention, using either human genomic DNA or cDNA as a template.

25     Alternatively, synthetic chemistry techniques can be used to synthesize lysosomal acid lipase polynucleotides. The degeneracy of the genetic code allows alternate nucleotide sequences to be synthesized which will encode a lysosomal acid lipase polypeptide having, for example, an amino acid sequence shown in SEQ ID NO:2, 5, 30     or 6 or a biologically active variant thereof.



Extending Polynucleotides

The partial sequence disclosed herein can be used to identify the corresponding full length gene from which it is derived. The partial sequences can be nick-translated or end-labeled with  $^{32}\text{P}$  using polynucleotide kinase using labeling methods known to those with skill in the art (BASIC METHODS IN MOLECULAR BIOLOGY, Davis *et al.*, eds., Elsevier Press, N.Y., 1986). A lambda library prepared from human tissue can be directly screened with the labeled sequences of interest or the library can be converted en masse to pBluescript (Stratagene Cloning Systems, La Jolla, Calif. 92037) to facilitate bacterial colony screening (see Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, Cold Spring Harbor Laboratory Press (1989, pg. 1.20).

Both methods are well known in the art. Briefly, filters with bacterial colonies containing the library in pBluescript or bacterial lawns containing lambda plaques are denatured, and the DNA is fixed to the filters. The filters are hybridized with the labeled probe using hybridization conditions described by Davis *et al.*, 1986. The partial sequences, cloned into lambda or pBluescript, can be used as positive controls to assess background binding and to adjust the hybridization and washing stringencies necessary for accurate clone identification. The resulting autoradiograms are compared to duplicate plates of colonies or plaques; each exposed spot corresponds to a positive colony or plaque. The colonies or plaques are selected, expanded and the DNA is isolated from the colonies for further analysis and sequencing.

Positive cDNA clones are analyzed to determine the amount of additional sequence they contain using PCR with one primer from the partial sequence and the other primer from the vector. Clones with a larger vector-insert PCR product than the original partial sequence are analyzed by restriction digestion and DNA sequencing to determine whether they contain an insert of the same size or similar as the mRNA size determined from Northern blot Analysis.

Once one or more overlapping cDNA clones are identified, the complete sequence of the clones can be determined, for example after exonuclease III digestion (McCombie *et al.*, *Methods* 3, 33-40, 1991). A series of deletion clones are generated, each of which is sequenced. The resulting overlapping sequences are assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a highly accurate final sequence.

Various PCR-based methods can be used to extend the nucleic acid sequences disclosed herein to detect upstream sequences such as promoters and regulatory elements. For example, restriction-site PCR uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, *PCR Methods Applic.* 2, 318-322, 1993). Genomic DNA is first amplified in the presence of a primer to a linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR also can be used to amplify or extend sequences using divergent primers based on a known region (Triglia *et al.*, *Nucleic Acids Res.* 16, 8186, 1988). Primers can be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, Minn.), to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72 °C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Another method which can be used is capture PCR, which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom *et al.*, *PCR Methods Applic.* 1, 111-119,

1991). In this method, multiple restriction enzyme digestions and ligations also can be used to place an engineered double-stranded sequence into an unknown fragment of the DNA molecule before performing PCR.

5 Another method which can be used to retrieve unknown sequences is that of Parker *et al.*, *Nucleic Acids Res.* 19, 3055-3060, 1991). Additionally, PCR, nested primers, and PROMOTERFINDER libraries (CLONTECH, Palo Alto, Calif.) can be used to walk genomic DNA (CLONTECH, Palo Alto, Calif.). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

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When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Randomly-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an  
15 oligo d(T) library does not yield a full-length cDNA. Genomic libraries can be useful for extension of sequence into 5' non-transcribed regulatory regions.

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Commercially available capillary electrophoresis systems can be used to analyze the size or confirm the nucleotide sequence of PCR or sequencing products. For  
example, capillary sequencing can employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity can be converted to electrical signal using appropriate software (e.g. GENOTYPER and Sequence NAVIGATOR, Perkin Elmer), and the  
25 entire process from loading of samples to computer analysis and electronic data display can be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample.

### Obtaining Polypeptides

Human lysosomal acid lipase polypeptides can be obtained, for example, by purification from human cells, by expression of lysosomal acid lipase polynucleotides, or by direct chemical synthesis.

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### Protein Purification

Human lysosomal acid lipase polypeptides can be purified from any cell which expresses the enzyme, including host cells which have been transfected with lysosomal acid lipase expression constructs. A purified lysosomal acid lipase polypeptide is separated from other compounds which normally associate with the lysosomal acid lipase polypeptide in the cell, such as certain proteins, carbohydrates, or lipids, using methods well-known in the art. Such methods include, but are not limited to, size exclusion chromatography, ammonium sulfate fractionation, ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis. A preparation of purified lysosomal acid lipase polypeptides is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure. Purity of the preparations can be assessed by any means known in the art, such as SDS-polyacrylamide gel electrophoresis.

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### Expression of Polynucleotides

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To express a lysosomal acid lipase polynucleotide, the polynucleotide can be inserted into an expression vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art can be used to construct expression vectors containing sequences encoding lysosomal acid lipase polypeptides and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook *et al.* (1989) and in Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, N.Y., 1989.

- A variety of expression vector/host systems can be utilized to contain and express sequences encoding a lysosomal acid lipase polypeptide. These include, but are not limited to, microorganisms, such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors, insect cell systems infected with virus expression vectors (e.g., baculovirus), plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids), or animal cell systems.
- The control elements or regulatory sequences are those non-translated regions of the vector — enhancers, promoters, 5' and 3' untranslated regions — which interact with host cellular proteins to carry out transcription and translation. Such elements can vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, can be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the BLUESCRIPT phagemid (Stratagene, LaJolla, Calif.) or pSPORT1 plasmid (Life Technologies) and the like can be used. The baculovirus polyhedrin promoter can be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (e.g., heat shock, RUBISCO, and storage protein genes) or from plant viruses (e.g., viral promoters or leader sequences) can be cloned into the vector. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of a nucleotide sequence encoding a lysosomal acid lipase polypeptide, vectors based on SV40 or EBV can be used with an appropriate selectable marker.

#### Bacterial and Yeast Expression Systems

- In bacterial systems, a number of expression vectors can be selected depending upon the use intended for the lysosomal acid lipase polypeptide. For example, when a large quantity of a lysosomal acid lipase polypeptide is needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are

readily purified can be used. Such vectors include, but are not limited to, multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene). In a BLUESCRIPT vector, a sequence encoding the lysosomal acid lipase polypeptide can be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of  $\beta$ -galactosidase so that a hybrid protein is produced. pIN vectors (Van Heeke & Schuster, *J. Biol. Chem.* 264, 5503-5509, 1989) or pGEX vectors (Promega, Madison, Wis.) also can be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems can be designed to include heparin, thrombin, or factor Xa protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH can be used. For reviews, see Ausubel *et al.* (1989) and Grant *et al.*, *Methods Enzymol.* 153, 516-544, 1987.

#### Plant and Insect Expression Systems

If plant expression vectors are used, the expression of sequences encoding lysosomal acid lipase polypeptides can be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV can be used alone or in combination with the omega leader sequence from TMV (Takamatsu, *EMBO J.* 6, 307-311, 1987). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters can be used (Coruzzi *et al.*, *EMBO J.* 3, 1671-1680, 1984; Broglie *et al.*, *Science* 224, 838-843, 1984; Winter *et al.*, *Results Probl. Cell Differ.* 17, 85-105, 1991). These constructs can be introduced into plant cells by direct DNA transformation or by pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (e.g., Hobbs or

Murray, in MCGRAW HILL YEARBOOK OF SCIENCE AND TECHNOLOGY, McGraw Hill, New York, N.Y., pp. 191-196, 1992).

5 An insect system also can be used to express a lysosomal acid lipase polypeptide. For example, in one such system *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. Sequences encoding lysosomal acid lipase polypeptides can be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of  
10 lysosomal acid lipase polypeptides will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses can then be used to infect *S. frugiperda* cells or *Trichoplusia* larvae in which lysosomal acid lipase polypeptides can be expressed (Engelhard *et al.*, *Proc. Nat. Acad. Sci.* 91, 3224-3227, 1994).

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#### Mammalian Expression Systems

A number of viral-based expression systems can be used to express lysosomal acid lipase polypeptides in mammalian host cells. For example, if an adenovirus is used as an expression vector, sequences encoding lysosomal acid lipase polypeptides can  
20 be ligated into an adenovirus transcription/translation complex comprising the late promoter and tripartite leader sequence. Insertion in a non-essential B1 or E3 region of the viral genome can be used to obtain a viable virus which is capable of expressing a lysosomal acid lipase polypeptide in infected host cells (Logan & Shenk, *Proc. Natl. Acad. Sci.* 81, 3655-3659, 1984). If desired, transcription  
25 enhancers, such as the Rous sarcoma virus (RSV) enhancer, can be used to increase expression in mammalian host cells.

Human artificial chromosomes (HACs) also can be used to deliver larger fragments of DNA than can be contained and expressed in a plasmid. HACs of 6M to 10M are  
30 constructed and delivered to cells via conventional delivery methods (*e.g.*, liposomes, polycationic amino polymers, or vesicles).

Specific initiation signals also can be used to achieve more efficient translation of sequences encoding lysosomal acid lipase polypeptides. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding a lysosomal acid lipase polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals (including the ATG initiation codon) should be provided. The initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used (see Scharf *et al.*, *Results Probl. Cell Differ.* 20, 125-162, 1994).

#### Host Cells

A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed lysosomal acid lipase polypeptide in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209) and can be chosen to ensure the correct modification and processing of the foreign protein.

Stable expression is preferred for long-term, high-yield production of recombinant proteins. For example, cell lines which stably express lysosomal acid lipase polypeptides can be transformed using expression vectors which can contain viral origins



of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells can be allowed to grow for 1-2 days in an enriched medium before they are switched to a selective medium. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced lysosomal acid lipase sequences. Resistant clones of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type. See, for example, ANIMAL CELL CULTURE, R.I. Freshney, ed., 1986.

Any number of selection systems can be used to recover transformed cell lines.

These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, *Cell* 11, 223-32, 1977) and adenine phosphoribosyltransferase (Lowy *et al.*, *Cell* 22, 817-23, 1980) genes which can be employed in *tk* or *aprt* cells, respectively. Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate (Wigler *et al.*, *Proc. Natl. Acad. Sci.* 77, 3567-70, 1980), *npt* confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin *et al.*, *J. Mol. Biol.* 150, 1-14, 1981), and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murray, 1992, *supra*). Additional selectable genes have been described. For example, *trpB* allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman & Mulligan, *Proc. Natl. Acad. Sci.* 85, 8047-51, 1988). Visible markers such as anthocyanins,  $\beta$ -glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, can be used to identify transformants and to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes *et al.*, *Methods Mol. Biol.* 55, 121-131, 1995).

#### Detecting Expression

Although the presence of marker gene expression suggests that the lysosomal acid lipase polynucleotide is also present, its presence and expression may need to be

confirmed. For example, if a sequence encoding a lysosomal acid lipase polypeptide is inserted within a marker gene sequence, transformed cells containing sequences which encode a lysosomal acid lipase polypeptide can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a  
5 sequence encoding a lysosomal acid lipase polypeptide under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the lysosomal acid lipase polynucleotide.

Alternatively, host cells which contain a lysosomal acid lipase polynucleotide and  
10 which express a lysosomal acid lipase polypeptide can be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip-based technologies for the detection and/or quantification of nucleic acid or protein. For  
15 example, the presence of a polynucleotide sequence encoding a lysosomal acid lipase polypeptide can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments of polynucleotides encoding a lysosomal acid lipase polypeptide. Nucleic acid amplification-based assays involve the use of oligonucleotides selected from sequences encoding a lysosomal acid lipase  
20 polypeptide to detect transformants which contain a lysosomal acid lipase polynucleotide.

A variety of protocols for detecting and measuring the expression of a lysosomal acid lipase polypeptide, using either polyclonal or monoclonal antibodies specific for the  
25 polypeptide, are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay using monoclonal antibodies reactive to two non-interfering epitopes on a lysosomal acid lipase polypeptide can be used, or a competitive binding assay can be employed. These and other assays are  
30 described in Hampton *et al.*, SEROLOGICAL METHODS: A LABORATORY MANUAL,

APS Press, St. Paul, Minn., 1990) and Maddox *et al.*, *J. Exp. Med.* 158, 1211-1216, 1983).

5 A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding lysosomal acid lipase polypeptides include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, sequences encoding a lysosomal acid lipase polypeptide can be cloned  
10 into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of labeled nucleotides and an appropriate RNA polymerase such as T7, T3, or SP6. These procedures can be conducted using a variety of commercially available kits (Amersham Pharmacia Biotech, Promega, and US Biochemical).  
15 Suitable reporter molecules or labels which can be used for ease of detection include radionuclides, enzymes, and fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

#### Expression and Purification of Polypeptides

20 Host cells transformed with nucleotide sequences encoding a lysosomal acid lipase polypeptide can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The polypeptide produced by a transformed cell can be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing  
25 polynucleotides which encode lysosomal acid lipase polypeptides can be designed to contain signal sequences which direct secretion of soluble lysosomal acid lipase polypeptides through a prokaryotic or eukaryotic cell membrane or which direct the membrane insertion of membrane-bound lysosomal acid lipase polypeptide.

30 As discussed above, other constructions can be used to join a sequence encoding a lysosomal acid lipase polypeptide to a nucleotide sequence encoding a polypeptide

domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). Inclusion of cleavable linker sequences such as those specific for Factor Xa or enterokinase (Invitrogen, San Diego, CA) between the purification domain and the lysosomal acid lipase polypeptide also can be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a lysosomal acid lipase polypeptide and 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification by IMAC (immobilized metal ion affinity chromatography, as described in Porath *et al.*, *Prot. Exp. Purif.* 3, 263-281, 1992), while the enterokinase cleavage site provides a means for purifying the lysosomal acid lipase polypeptide from the fusion protein. Vectors which contain fusion proteins are disclosed in Kroll *et al.*, *DNA Cell Biol.* 12, 441-453, 1993.

#### Chemical Synthesis

Sequences encoding a lysosomal acid lipase polypeptide can be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers *et al.*, *Nucl. Acids Res. Symp. Ser.* 215-223, 1980; Horn *et al.* *Nucl. Acids Res. Symp. Ser.* 225-232, 1980). Alternatively, a lysosomal acid lipase polypeptide itself can be produced using chemical methods to synthesize its amino acid sequence, such as by direct peptide synthesis using solid-phase techniques (Merrifield, *J. Am. Chem. Soc.* 85, 2149-2154, 1963; Roberge *et al.*, *Science* 269, 202-204, 1995). Protein synthesis can be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Optionally, fragments of lysosomal acid lipase polypeptides can be separately synthesized and combined using chemical methods to produce a full-length molecule.

The newly synthesized peptide can be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES, WH Freeman and Co., New York, N.Y., 1983). The composition of a synthetic lysosomal acid lipase polypeptide can be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; see Creighton, *supra*). Additionally, any portion of the amino acid sequence of the lysosomal acid lipase polypeptide can be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins to produce a variant polypeptide or a fusion protein.

#### Production of Altered Polypeptides

As will be understood by those of skill in the art, it may be advantageous to produce lysosomal acid lipase polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences disclosed herein can be engineered using methods generally known in the art to alter lysosomal acid lipase polypeptide-encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the polypeptide or mRNA product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides can be used to engineer the nucleotide sequences. For example, site-directed mutagenesis can be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

Antibodies

- Any type of antibody known in the art can be generated to bind specifically to an epitope of a lysosomal acid lipase polypeptide. "Antibody" as used herein includes intact immunoglobulin molecules, as well as fragments thereof, such as Fab, F(ab')<sub>2</sub>, and Fv, which are capable of binding an epitope of a lysosomal acid lipase polypeptide. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids.
- 10 An antibody which specifically binds to an epitope of a lysosomal acid lipase polypeptide can be used therapeutically, as well as in immunochemical assays, such as Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art. Various immunoassays can be used to identify antibodies having the desired specificity.
- 15 Numerous protocols for competitive binding or immunoradiometric assays are well known in the art. Such immunoassays typically involve the measurement of complex formation between an immunogen and an antibody which specifically binds to the immunogen.
- 20 Typically, an antibody which specifically binds to a lysosomal acid lipase polypeptide provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in an immunochemical assay. Preferably, antibodies which specifically bind to lysosomal acid lipase polypeptides do not detect other proteins in immunochemical assays and can
- 25 immunoprecipitate a lysosomal acid lipase polypeptide from solution.
- Human lysosomal acid lipase polypeptides can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, a lysosomal acid lipase polypeptide can be conjugated to a carrier protein, such as bovine serum albumin, thyroglobulin, and keyhole limpet hemo-
- 30 cyanin. Depending on the host species, various adjuvants can be used to increase the

- 30 -

immunological response. Such adjuvants include, but are not limited to, Freund's adjuvant, mineral gels (e.g., aluminum hydroxide), and surface active substances (e.g. lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol). Among adjuvants used in humans, BCG  
5 (*bacilli Calmette-Guerin*) and *Corynebacterium parvum* are especially useful.

Monoclonal antibodies which specifically bind to a lysosomal acid lipase polypeptide can be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These techniques include, but are not  
10 limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler *et al.*, *Nature* 256, 495-497, 1985; Kozbor *et al.*, *J. Immunol. Methods* 81, 31-42, 1985; Cote *et al.*, *Proc. Natl. Acad. Sci.* 80, 2026-2030, 1983; Cole *et al.*, *Mol. Cell Biol.* 62, 109-120, 1984).

15 In addition, techniques developed for the production of "chimeric antibodies," the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison *et al.*, *Proc. Natl. Acad. Sci.* 81, 6851-6855, 1984; Neuberger *et al.*, *Nature* 312, 604-608, 1984; Takeda *et al.*, *Nature* 314, 452-454, 1985). Monoclonal and other antibodies  
20 also can be "humanized" to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues. Sequence differences between rodent antibodies and human sequences can be minimized by replacing residues which  
25 differ from those in the human sequences by site directed mutagenesis of individual residues or by grating of entire complementarity determining regions. Alternatively, humanized antibodies can be produced using recombinant methods, as described in GB2188638B. Antibodies which specifically bind to a lysosomal acid lipase polypeptide can contain antigen binding sites which are either partially or fully  
30 humanized, as disclosed in U.S. 5,565,332.

Alternatively, techniques described for the production of single chain antibodies can be adapted using methods known in the art to produce single chain antibodies which specifically bind to lysosomal acid lipase polypeptides. Antibodies with related specificity, but of distinct idiotypic composition, can be generated by chain shuffling from random combinatorial immunoglobulin libraries (Burton, *Proc. Natl. Acad. Sci.* 88, 11120-23, 1991).

Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, 1996, *Eur. J. Cancer Prev.* 5, 507-11). Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for example, in Coloma & Morrison, 1997, *Nat. Biotechnol.* 15, 159-63. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender & Voss, 1994, *J. Biol. Chem.* 269, 199-206.

A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology (Verhaar *et al.*, 1995, *Int. J. Cancer* 61, 497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth.* 165, 81-91).

Antibodies which specifically bind to lysosomal acid lipase polypeptides also can be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi *et al.*, *Proc. Natl. Acad. Sci.* 86, 3833-3837, 1989; Winter *et al.*, *Nature* 349, 293-299, 1991).

Other types of antibodies can be constructed and used therapeutically in methods of the invention. For example, chimeric antibodies can be constructed as disclosed in



WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, also can be prepared.

5 Antibodies according to the invention can be purified by methods well known in the art. For example, antibodies can be affinity purified by passage over a column to which a lysosomal acid lipase polypeptide is bound. The bound antibodies can then be eluted from the column using a buffer with a high salt concentration.

10 Antisense Oligonucleotides

Antisense oligonucleotides are nucleotide sequences which are complementary to a specific DNA or RNA sequence. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form complexes and block either transcription or translation. Preferably, an antisense oligonucleotide is at least 11 nucleotides in length, but can be at least 12, 15, 20, 25, 30, 35, 40, 45, 15 or 50 or more nucleotides long. Longer sequences also can be used. Antisense oligonucleotide molecules can be provided in a DNA construct and introduced into a cell as described above to decrease the level of lysosomal acid lipase gene products in the cell.

20 Antisense oligonucleotides can be deoxyribonucleotides, ribonucleotides, or a combination of both. Oligonucleotides can be synthesized manually or by an automated synthesizer, by covalently linking the 5' end of one nucleotide with the 3' end of another nucleotide with non-phosphodiester internucleotide linkages such 25 alkylphosphonates, phosphorothioates, phosphorodithioates, alkylphosphonothioates, alkylphosphonates, phosphoramidates, phosphate esters, carbamates, acetamidate, carboxymethyl esters, carbonates, and phosphate triesters. See Brown, *Meth. Mol. Biol.* 20, 1-8, 1994; Sonveaux, *Meth. Mol. Biol.* 26, 1-72, 1994; Uhlmann *et al.*, *Chem. Rev.* 90, 543-583, 1990.

Modifications of lysosomal acid lipase gene expression can be obtained by designing antisense oligonucleotides which will form duplexes to the control, 5', or regulatory regions of the lysosomal acid lipase gene. Oligonucleotides derived from the transcription initiation site, *e.g.*, between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or chaperons. Therapeutic advances using triplex DNA have been described in the literature (*e.g.*, Gee *et al.*, in Huber & Carr, MOLECULAR AND IMMUNOLOGIC APPROACHES, Futura Publishing Co., Mt. Kisco, N.Y., 1994). An antisense oligonucleotide also can be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Precise complementarity is not required for successful complex formation between an antisense oligonucleotide and the complementary sequence of a lysosomal acid lipase polynucleotide. Antisense oligonucleotides which comprise, for example, 2, 3, 4, or 5 or more stretches of contiguous nucleotides which are precisely complementary to a lysosomal acid lipase polynucleotide, each separated by a stretch of contiguous nucleotides which are not complementary to adjacent lysosomal acid lipase nucleotides, can provide sufficient targeting specificity for lysosomal acid lipase mRNA. Preferably, each stretch of complementary contiguous nucleotides is at least 4, 5, 6, 7, or 8 or more nucleotides in length. Non-complementary intervening sequences are preferably 1, 2, 3, or 4 nucleotides in length. One skilled in the art can easily use the calculated melting point of an antisense-sense pair to determine the degree of mismatching which will be tolerated between a particular antisense oligonucleotide and a particular lysosomal acid lipase polynucleotide sequence.

Antisense oligonucleotides can be modified without affecting their ability to hybridize to a lysosomal acid lipase polynucleotide. These modifications can be internal or at one or both ends of the antisense molecule. For example,

internucleoside phosphate linkages can be modified by adding cholesteryl or diamine moieties with varying numbers of carbon residues between the amino groups and terminal ribose. Modified bases and/or sugars, such as arabinose instead of ribose, or a 3', 5'-substituted oligonucleotide in which the 3' hydroxyl group or the 5' phosphate group are substituted, also can be employed in a modified antisense oligonucleotide. These modified oligonucleotides can be prepared by methods well known in the art. See, e.g., Agrawal *et al.*, *Trends Biotechnol.* 10, 152-158, 1992; Uhlmann *et al.*, *Chem. Rev.* 90, 543-584, 1990; Uhlmann *et al.*, *Tetrahedron. Lett.* 215, 3539-3542, 1987.

### Ribozymes

Ribozymes are RNA molecules with catalytic activity. See, e.g., Cech, *Science* 236, 1532-1539; 1987; Cech, *Ann. Rev. Biochem.* 59, 543-568; 1990, Cech, *Curr. Opin. Struct. Biol.* 2, 605-609; 1992, Couture & Stinchcomb, *Trends Genet.* 12, 510-515, 1996. Ribozymes can be used to inhibit gene function by cleaving an RNA sequence, as is known in the art (e.g., Haseloff *et al.*, U.S. Patent 5,641,673). The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Examples include engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of specific nucleotide sequences.

The coding sequence of a lysosomal acid lipase polynucleotide can be used to generate ribozymes which will specifically bind to mRNA transcribed from the lysosomal acid lipase polynucleotide. Methods of designing and constructing ribozymes which can cleave other RNA molecules in trans in a highly sequence specific manner have been developed and described in the art (see Haseloff *et al.* *Nature* 334, 585-591, 1988). For example, the cleavage activity of ribozymes can be targeted to specific RNAs by engineering a discrete "hybridization" region into the ribozyme. The hybridization region contains a sequence complementary to the target

RNA and thus specifically hybridizes with the target (see, for example, Gerlach *et al.*, EP 321,201).

5 Specific ribozyme cleavage sites within a lysosomal acid lipase RNA target can be identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target RNA containing the cleavage site can be evaluated for secondary structural features which may render the target inoperable. Suitability of candidate lysosomal  
10 acid lipase RNA targets also can be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays. Longer complementary sequences can be used to increase the affinity of the hybridization sequence for the target. The hybridizing and cleavage regions of the ribozyme can be integrally related such that upon hybridizing to the target RNA through the  
15 complementary regions, the catalytic region of the ribozyme can cleave the target.

Ribozymes can be introduced into cells as part of a DNA construct. Mechanical methods, such as microinjection, liposome-mediated transfection, electroporation, or calcium phosphate precipitation, can be used to introduce a ribozyme-containing  
20 DNA construct into cells in which it is desired to decrease lysosomal acid lipase expression. Alternatively, if it is desired that the cells stably retain the DNA construct, the construct can be supplied on a plasmid and maintained as a separate element or integrated into the genome of the cells, as is known in the art. A ribozyme-encoding DNA construct can include transcriptional regulatory elements,  
25 such as a promoter element, an enhancer or UAS element, and a transcriptional terminator signal, for controlling transcription of ribozymes in the cells.

As taught in Haseloff *et al.*, U.S. Patent 5,641,673, ribozymes can be engineered so that ribozyme expression will occur in response to factors which induce expression  
30 of a target gene. Ribozymes also can be engineered to provide an additional level of

regulation, so that destruction of mRNA occurs only when both a ribozyme and a target gene are induced in the cells.

#### Differentially Expressed Genes

5 Described herein are methods for the identification of genes whose products interact with human lysosomal acid lipase. Such genes may represent genes which are differentially expressed in disorders including, but not limited to, cancer, CNS disorders, obesity, COPD, diabetes, and cardiovascular disorders. Further, such genes may represent genes which are differentially regulated in response to  
10 manipulations relevant to the progression or treatment of such diseases. Additionally, such genes may have a temporally modulated expression, increased or decreased at different stages of tissue or organism development. A differentially expressed gene may also have its expression modulated under control versus experimental conditions. In addition, the human lysosomal acid lipase gene or gene  
15 product may itself be tested for differential expression.

The degree to which expression differs in a normal versus a diseased state need only be large enough to be visualized via standard characterization techniques such as differential display techniques. Other such standard characterization techniques by  
20 which expression differences may be visualized include but are not limited to, quantitative RT (reverse transcriptase), PCR, and Northern analysis.

#### Identification of Differentially Expressed Genes

To identify differentially expressed genes total RNA or, preferably, mRNA is  
25 isolated from tissues of interest. For example, RNA samples are obtained from tissues of experimental subjects and from corresponding tissues of control subjects. Any RNA isolation technique which does not select against the isolation of mRNA may be utilized for the purification of such RNA samples. See, for example, Ausubel *et al.*, ed., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, Inc.  
30 New York, 1987-1993. Large numbers of tissue samples may readily be processed

using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski, U.S. Patent 4,843,155.

5 Transcripts within the collected RNA samples which represent RNA produced by differentially expressed genes are identified by methods well known to those of skill in the art. They include, for example, differential screening (Tedder *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 85, 208-12, 1988), subtractive hybridization (Hedrick *et al.*, *Nature* 308, 149-53; Lee *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 88, 2825, 1984), and, preferably, differential display (Liang & Pardee, *Science* 257, 967-71, 1992; U.S. Patent 5,262,311).

15 The differential expression information may itself suggest relevant methods for the treatment of disorders involving the human lysosomal acid lipase. For example, treatment may include a modulation of expression of the differentially expressed genes and/or the gene encoding the human lysosomal acid lipase. The differential expression information may indicate whether the expression or activity of the differentially expressed gene or gene product or the human lysosomal acid lipase gene or gene product are up-regulated or down-regulated.

#### 20 Screening Methods

The invention provides assays for screening test compounds which bind to or modulate the activity of a lysosomal acid lipase polypeptide or a lysosomal acid lipase polynucleotide. A test compound preferably binds to a lysosomal acid lipase polypeptide or polynucleotide. More preferably, a test compound decreases or increases lipase activity by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the test compound.

#### Test Compounds

30 Test compounds can be pharmacologic agents already known in the art or can be compounds previously unknown to have any pharmacological activity. The compounds can be naturally occurring or designed in the laboratory. They can be

isolated from microorganisms, animals, or plants, and can be produced recombinantly, or synthesized by chemical methods known in the art. If desired, test compounds can be obtained using any of the numerous combinatorial library methods known in the art, including but not limited to, biological libraries, spatially  
5 addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer, or small molecule libraries of  
10 compounds. See Lam, *Anticancer Drug Des.* 12, 145, 1997.

Methods for the synthesis of molecular libraries are well known in the art (see, for example, DeWitt *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 90, 6909, 1993; Erb *et al.* *Proc. Natl. Acad. Sci. U.S.A.* 91, 11422, 1994; Zuckermann *et al.*, *J. Med. Chem.* 37, 2678,  
15 1994; Cho *et al.*, *Science* 261, 1303, 1993; Carell *et al.*, *Angew. Chem. Int. Ed. Engl.* 33, 2059, 1994; Carell *et al.*, *Angew. Chem. Int. Ed. Engl.* 33, 2061; Gallop *et al.*, *J. Med. Chem.* 37, 1233, 1994). Libraries of compounds can be presented in solution (see, e.g., Houghten, *BioTechniques* 13, 412-421, 1992), or on beads (Lam, *Nature* 354, 82-84, 1991), chips (Fodor, *Nature* 364, 555-556, 1993), bacteria or spores  
20 (Ladner, U.S. Patent 5,223,409), plasmids (Cull *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 89, 1865-1869, 1992), or phage (Scott & Smith, *Science* 249, 386-390, 1990; Devlin, *Science* 249, 404-406, 1990); Cwirla *et al.*, *Proc. Natl. Acad. Sci.* 97, 6378-6382, 1990; Felici, *J. Mol. Biol.* 222, 301-310, 1991; and Ladner, U.S. Patent 5,223,409).

### 25 High Throughput Screening

Test compounds can be screened for the ability to bind to lysosomal acid lipase polypeptides or polynucleotides or to affect lysosomal acid lipase activity or lysosomal acid lipase gene expression using high throughput screening. Using high  
30 throughput screening, many discrete compounds can be tested in parallel so that large numbers of test compounds can be quickly screened. The most widely established techniques utilize 96-well microtiter plates. The wells of the microtiter plates

typically require assay volumes that range from 50 to 500  $\mu$ l. In addition to the plates, many instruments, materials, pipettors, robotics, plate washers, and plate readers are commercially available to fit the 96-well format.

- 5 Alternatively, "free format assays," or assays that have no physical barrier between samples, can be used. For example, an assay using pigment cells (melanocytes) in a simple homogeneous assay for combinatorial peptide libraries is described by Jayawickreme *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 19, 1614-18 (1994). The cells are placed under agarose in petri dishes, then beads that carry combinatorial compounds are placed on the surface of the agarose. The combinatorial compounds are partially released the compounds from the beads. Active compounds can be visualized as dark pigment areas because, as the compounds diffuse locally into the gel matrix, the active compounds cause the cells to change colors.
- 10
- 15 Another example of a free format assay is described by Chelsky, "Strategies for Screening Combinatorial Libraries: Novel and Traditional Approaches," reported at the First Annual Conference of The Society for Biomolecular Screening in Philadelphia, Pa. (Nov. 7-10, 1995). Chelsky placed a simple homogenous enzyme assay for carbonic anhydrase inside an agarose gel such that the enzyme in the gel would cause a color change throughout the gel. Thereafter, beads carrying combinatorial compounds via a photolinker are placed inside the gel and the compounds are partially released by UV-light. Compounds that inhibited the enzyme are observed as local zones of inhibition having less color change.
- 20
- 25 Yet another example is described by Salmon *et al.*, *Molecular Diversity* 2, 57-63 (1996). In this example, combinatorial libraries are screened for compounds that had cytotoxic effects on cancer cells growing in agar.

- Another high throughput screening method is described in Beutel *et al.*, U.S. Patent 5,976,813. In this method, test samples are placed in a porous matrix. One or more assay components are then placed within, on top of, or at the bottom of a matrix such
- 30



as a gel, a plastic sheet, a filter, or other form of easily manipulated solid support. When samples are introduced to the porous matrix they diffuse sufficiently slowly, such that the assays can be performed without the test samples running together.

5     Binding Assays

For binding assays, the test compound is preferably a small molecule which binds to and occupies, for example, the active site of the lysosomal acid lipase polypeptide, such that normal biological activity is prevented. Examples of such small molecules include, but are not limited to, small peptides or peptide-like molecules.

10

In binding assays, either the test compound or the lysosomal acid lipase polypeptide can comprise a detectable label, such as a fluorescent, radioisotopic, chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase. Detection of a test compound which is bound to the  
15     lysosomal acid lipase polypeptide can then be accomplished, for example, by direct counting of radioemmission, by scintillation counting, or by determining conversion of an appropriate substrate to a detectable product.

20

Alternatively, binding of a test compound to a lysosomal acid lipase polypeptide can be determined without labeling either of the interactants. For example, a microphysiometer can be used to detect binding of a test compound with a lysosomal acid lipase polypeptide. A microphysiometer (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate  
25     can be used as an indicator of the interaction between a test compound and a lysosomal acid lipase polypeptide (McConnell *et al.*, *Science* 257, 1906-1912, 1992).

30

Determining the ability of a test compound to bind to a lysosomal acid lipase polypeptide also can be accomplished using a technology such as real-time Bimolecular Interaction Analysis (BIA) (Sjolander & Urbaniczky, *Anal. Chem.* 63, 2338-2345, 1991, and Szabo *et al.*, *Curr. Opin. Struct. Biol.* 5, 699-705, 1995). BIA

is a technology for studying biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcore<sup>TM</sup>). Changes in the optical phenomenon surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

5

In yet another aspect of the invention, a lysosomal acid lipase polypeptide can be used as a "bait protein" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent 5,283,317; Zervos *et al.*, *Cell* 72, 223-232, 1993; Madura *et al.*, *J. Biol. Chem.* 268, 12046-12054, 1993; Bartel *et al.*, *BioTechniques* 14, 920-924, 1993; Iwabuchi *et al.*, *Oncogene* 8, 1693-1696, 1993; and Brent W094/10300), to identify other  
10 proteins which bind to or interact with the lysosomal acid lipase polypeptide and modulate its activity.

15

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. For example, in one construct, polynucleotide encoding a lysosomal acid lipase polypeptide can be fused to a polynucleotide encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct a DNA sequence that encodes an unidentified protein ("prey" or  
20 "sample") can be fused to a polynucleotide that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact *in vivo* to form an protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ), which is operably  
25 linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the DNA sequence encoding the protein which interacts with the lysosomal acid lipase polypeptide.

30

It may be desirable to immobilize either the lysosomal acid lipase polypeptide (or polynucleotide) or the test compound to facilitate separation of bound from unbound

forms of one or both of the interactants, as well as to accommodate automation of the assay. Thus, either the lysosomal acid lipase polypeptide (or polynucleotide) or the test compound can be bound to a solid support. Suitable solid supports include, but are not limited to, glass or plastic slides, tissue culture plates, microtiter wells, tubes, silicon chips, or particles such as beads (including, but not limited to, latex, polystyrene, or glass beads). Any method known in the art can be used to attach the enzyme polypeptide (or polynucleotide) or test compound to a solid support, including use of covalent and non-covalent linkages, passive absorption, or pairs of binding moieties attached respectively to the polypeptide (or polynucleotide) or test compound and the solid support. Test compounds are preferably bound to the solid support in an array, so that the location of individual test compounds can be tracked. Binding of a test compound to a lysosomal acid lipase polypeptide (or polynucleotide) can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes.

In one embodiment, the lysosomal acid lipase polypeptide is a fusion protein comprising a domain that allows the lysosomal acid lipase polypeptide to be bound to a solid support. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and the non-adsorbed lysosomal acid lipase polypeptide; the mixture is then incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components. Binding of the interactants can be determined either directly or indirectly, as described above. Alternatively, the complexes can be dissociated from the solid support before binding is determined.

Other techniques for immobilizing proteins or polynucleotides on a solid support also can be used in the screening assays of the invention. For example, either a lysosomal

acid lipase polypeptide (or polynucleotide) or a test compound can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated lysosomal acid lipase polypeptides (or polynucleotides) or test compounds can be prepared from biotin-NHS(N-hydroxysuccinimide) using techniques well known in the art (e.g.,  
5 biotinylation kit, Pierce Chemicals, Rockford, Ill.) and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies which specifically bind to a lysosomal acid lipase polypeptide, polynucleotide, or a test compound, but which do not interfere with a desired binding site, such as the active site of the lysosomal acid lipase polypeptide, can be derivatized to the wells of the  
10 plate. Unbound target or protein can be trapped in the wells by antibody conjugation.

Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies which specifically bind to the lysosomal acid lipase polypeptide or test  
15 compound, enzyme-linked assays which rely on detecting an activity of the lysosomal acid lipase polypeptide, and SDS gel electrophoresis under non-reducing conditions.

Screening for test compounds which bind to a lysosomal acid lipase polypeptide or  
20 polynucleotide also can be carried out in an intact cell. Any cell which comprises a lysosomal acid lipase polypeptide or polynucleotide can be used in a cell-based assay system. A lysosomal acid lipase polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Binding of the test compound to a lysosomal acid lipase polypeptide or polynucleotide is  
25 determined as described above.

#### Enzyme Assays

Test compounds can be tested for the ability to increase or decrease the lipase activity of a human lysosomal acid lipase polypeptide. Lipase activity can be  
30 measured as is known in the art and described, for example, in Example 4, below.

Enzyme assays can be carried out after contacting either a purified lysosomal acid lipase polypeptide, a cell membrane preparation, or an intact cell with a test compound. A test compound which decreases a lipase activity of a lysosomal acid lipase polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential therapeutic agent for decreasing lysosomal acid lipase activity. A test compound which increases a lipase activity of a human lysosomal acid lipase polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential therapeutic agent for increasing human lysosomal acid lipase activity.

10

#### Gene Expression

In another embodiment, test compounds which increase or decrease lysosomal acid lipase gene expression are identified. A lysosomal acid lipase polynucleotide is contacted with a test compound, and the expression of an RNA or polypeptide product of the lysosomal acid lipase polynucleotide is determined. The level of expression of appropriate mRNA or polypeptide in the presence of the test compound is compared to the level of expression of mRNA or polypeptide in the absence of the test compound. The test compound can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater in the presence of the test compound than in its absence, the test compound is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less in the presence of the test compound than in its absence, the test compound is identified as an inhibitor of the mRNA or polypeptide expression.

25

The level of lysosomal acid lipase mRNA or polypeptide expression in the cells can be determined by methods well known in the art for detecting mRNA or polypeptide. Either qualitative or quantitative methods can be used. The presence of polypeptide products of a lysosomal acid lipase polynucleotide can be determined, for example, using a variety of techniques known in the art, including immunochemical methods such as radioimmunoassay, Western blotting, and immunohistochemistry.

30

Alternatively, polypeptide synthesis can be determined *in vivo*, in a cell culture, or in an *in vitro* translation system by detecting incorporation of labeled amino acids into a lysosomal acid lipase polypeptide.

- 5 Such screening can be carried out either in a cell-free assay system or in an intact cell. Any cell which expresses a lysosomal acid lipase polynucleotide can be used in a cell-based assay system. The lysosomal acid lipase polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Either a primary culture or an established cell line, such as CHO or human  
10 embryonic kidney 293 cells, can be used.

#### Pharmaceutical Compositions

- The invention also provides pharmaceutical compositions which can be administered to a patient to achieve a therapeutic effect. Pharmaceutical compositions of the  
15 invention can comprise, for example, a lysosomal acid lipase polypeptide, lysosomal acid lipase polynucleotide, ribozymes or antisense oligonucleotides, antibodies which specifically bind to a lysosomal acid lipase polypeptide, or mimetics, activators, or inhibitors of a lysosomal acid lipase polypeptide activity. The compositions can be administered alone or in combination with at least one other agent, such as stabilizing  
20 compound, which can be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions can be administered to a patient alone, or in combination with other agents, drugs or hormones.

- 25 In addition to the active ingredients, these pharmaceutical compositions can contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Pharmaceutical compositions of the invention can be administered by any number of routes including, but not limited to, oral, intravenous,  
30 intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, parenteral, topical, sublingual, or rectal

means. Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents can be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores can be used in conjunction with suitable coatings, such as concentrated sugar solutions, which also can contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments can be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, *i.e.*, dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds can be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration can be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions can contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds can be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Non-lipid polycationic amino polymers also can be used for delivery. Optionally, the suspension also can contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention can be manufactured in a manner that is known in the art, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes. The pharmaceutical composition can be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation can be a lyophilized powder which can contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

Further details on techniques for formulation and administration can be found in the latest edition of REMINGTON'S PHARMACEUTICAL SCIENCES (Maack Publishing Co., Easton, Pa.). After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated



condition. Such labeling would include amount, frequency, and method of administration.

Therapeutic Indications and Methods

5 Human lysosomal acid lipase can be regulated to treat cancer, CNS disorders, obesity, COPD, diabetes, and cardiovascular disorders.

Cancer is a disease fundamentally caused by oncogenic cellular transformation. There are several hallmarks of transformed cells that distinguish them from their  
10 normal counterparts and underlie the pathophysiology of cancer. These include uncontrolled cellular proliferation, unresponsiveness to normal death-inducing signals (immortalization), increased cellular motility and invasiveness, increased ability to recruit blood supply through induction of new blood vessel formation (angiogenesis), genetic instability, and dysregulated gene expression. Various  
15 combinations of these aberrant physiologies, along with the acquisition of drug-resistance frequently lead to an intractable disease state in which organ failure and patient death ultimately ensue.

Most standard cancer therapies target cellular proliferation and rely on the  
20 differential proliferative capacities between transformed and normal cells for their efficacy. This approach is hindered by the facts that several important normal cell types are also highly proliferative and that cancer cells frequently become resistant to these agents. Thus, the therapeutic indices for traditional anti-cancer therapies rarely exceed 2.0.

25 The advent of genomics-driven molecular target identification has opened up the possibility of identifying new cancer-specific targets for therapeutic intervention that will provide safer, more effective treatments for cancer patients. Thus, newly discovered tumor-associated genes and their products can be tested for their role(s) in  
30 disease and used as tools to discover and develop innovative therapies. Genes

playing important roles in any of the physiological processes outlined above can be characterized as cancer targets.

5 Genes or gene fragments identified through genomics can readily be expressed in one or more heterologous expression systems to produce functional recombinant proteins. These proteins are characterized *in vitro* for their biochemical properties and then used as tools in high-throughput molecular screening programs to identify chemical modulators of their biochemical activities. Agonists and/or antagonists of target protein activity can be identified in this manner and subsequently tested in cellular and *in vivo* disease models for anti-cancer activity. Optimization of lead compounds with iterative testing in biological models and detailed pharmacokinetic and toxicological analyses form the basis for drug development and subsequent testing in humans.

15 Obesity and overweight are defined as an excess of body fat relative to lean body mass. An increase in caloric intake or a decrease in energy expenditure or both can bring about this imbalance leading to surplus energy being stored as fat. Obesity is associated with important medical morbidities and an increase in mortality. The causes of obesity are poorly understood and may be due to genetic factors, environmental factors or a combination of the two to cause a positive energy balance. In contrast, anorexia and cachexia are characterized by an imbalance in energy intake versus energy expenditure leading to a negative energy balance and weight loss. Agents that either increase energy expenditure and/or decrease energy intake, absorption or storage would be useful for treating obesity, overweight, and associated comorbidities. Agents that either increase energy intake and/or decrease energy expenditure or increase the amount of lean tissue would be useful for treating cachexia, anorexia and wasting disorders.

30 This gene, translated proteins and agents which modulate this gene or portions of the gene or its products are useful for treating obesity, overweight, anorexia, cachexia, wasting disorders, appetite suppression, appetite enhancement, increases or decreases

in satiety, modulation of body weight, and/or other eating disorders such as bulimia. Also this gene, translated proteins and agents which modulate this gene or portions of the gene or its products are useful for treating obesity/overweight-associated comorbidities including hypertension, type 2 diabetes, coronary artery disease, hyperlipidemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea and respiratory problems, some types of cancer including endometrial, breast, prostate, and colon cancer, thrombotic disease, polycystic ovarian syndrome, reduced fertility, complications of pregnancy, menstrual irregularities, hirsutism, stress incontinence, and depression.

Chronic obstructive pulmonary (or airways) disease (COPD) is a condition defined physiologically as airflow obstruction that generally results from a mixture of emphysema and peripheral airway obstruction due to chronic bronchitis (Senior & Shapiro, *Pulmonary Diseases and Disorders*, 3d ed., New York, McGraw-Hill, 1998, pp. 659-681, 1998; Barnes, *Chest* 117, 10S-14S, 2000). Emphysema is characterized by destruction of alveolar walls leading to abnormal enlargement of the air spaces of the lung. Chronic bronchitis is defined clinically as the presence of chronic productive cough for three months in each of two successive years. In COPD, airflow obstruction is usually progressive and is only partially reversible. By far the most important risk factor for development of COPD is cigarette smoking, although the disease does occur in non-smokers.

Chronic inflammation of the airways is a key pathological feature of COPD (Senior & Shapiro, 1998). The inflammatory cell population comprises increased numbers of macrophages, neutrophils, and CD8<sup>+</sup> lymphocytes. Inhaled irritants, such as cigarette smoke, activate macrophages which are resident in the respiratory tract, as well as epithelial cells leading to release of chemokines (*e.g.*, interleukin-8) and other chemotactic factors. These chemotactic factors act to increase the neutrophil/monocyte trafficking from the blood into the lung tissue and airways. Neutrophils and monocytes recruited into the airways can release a variety of potentially damaging mediators such as proteolytic enzymes and reactive oxygen

species. Matrix degradation and emphysema, along with airway wall thickening, surfactant dysfunction, and mucus hypersecretion, all are potential sequelae of this inflammatory response that lead to impaired airflow and gas exchange.

5 Diabetes mellitus is a common metabolic disorder characterized by an abnormal elevation in blood glucose, alterations in lipids and abnormalities (complications) in the cardiovascular system, eye, kidney and nervous system. Diabetes is divided into two separate diseases: type 1 diabetes (juvenile onset), which results from a loss of cells which make and secrete insulin, and type 2 diabetes (adult onset), which is  
10 caused by a defect in insulin secretion and a defect in insulin action.

Type 1 diabetes is initiated by an autoimmune reaction that attacks the insulin secreting cells (beta cells) in the pancreatic islets. Agents that prevent this reaction from occurring or that stop the reaction before destruction of the beta cells has been  
15 accomplished are potential therapies for this disease. Other agents that induce beta cell proliferation and regeneration also are potential therapies.

Type II diabetes is the most common of the two diabetic conditions (6% of the population). The defect in insulin secretion is an important cause of the diabetic  
20 condition and results from an inability of the beta cell to properly detect and respond to rises in blood glucose levels with insulin release. Therapies that increase the response by the beta cell to glucose would offer an important new treatment for this disease.

25 The defect in insulin action in Type II diabetic subjects is another target for therapeutic intervention. Agents that increase the activity of the insulin receptor in muscle, liver, and fat will cause a decrease in blood glucose and a normalization of plasma lipids. The receptor activity can be increased by agents that directly stimulate the receptor or that increase the intracellular signals from the receptor. Other  
30 therapies can directly activate the cellular end process, *i.e.* glucose transport or various enzyme systems, to generate an insulin-like effect and therefore a produce

- 52 -

beneficial outcome. Because overweight subjects have a greater susceptibility to Type II diabetes, any agent that reduces body weight is a possible therapy.

5 Both Type I and Type diabetes can be treated with agents that mimic insulin action or that treat diabetic complications by reducing blood glucose levels. Likewise, agents that reduces new blood vessel growth can be used to treat the eye complications that develop in both diseases.

10 Cardiovascular diseases include the following disorders of the heart and the vascular system: congestive heart failure, myocardial infarction, ischemic diseases of the heart, all kinds of atrial and ventricular arrhythmias, hypertensive vascular diseases, and peripheral vascular diseases.

15 Heart failure is defined as a pathophysiologic state in which an abnormality of cardiac function is responsible for the failure of the heart to pump blood at a rate commensurate with the requirement of the metabolizing tissue. It includes all forms of pumping failure, such as high-output and low-output, acute and chronic, right-sided or left-sided, systolic or diastolic, independent of the underlying cause.

20 Myocardial infarction (MI) is generally caused by an abrupt decrease in coronary blood flow that follows a thrombotic occlusion of a coronary artery previously narrowed by arteriosclerosis. MI prophylaxis (primary and secondary prevention) is included, as well as the acute treatment of MI and the prevention of complications.

25 Ischemic diseases are conditions in which the coronary flow is restricted resulting in a perfusion which is inadequate to meet the myocardial requirement for oxygen. This group of diseases includes stable angina, unstable angina, and asymptomatic ischemia.

30 Arrhythmias include all forms of atrial and ventricular tachyarrhythmias (atrial tachycardia, atrial flutter, atrial fibrillation, atrio-ventricular reentrant tachycardia,

- 53 -

preexcitation syndrome, ventricular tachycardia, ventricular flutter, and ventricular fibrillation), as well as bradycardic forms of arrhythmias.

5       Hypertensive vascular diseases include primary as well as all kinds of secondary arterial hypertension (renal, endocrine, neurogenic, others). The disclosed gene and its product may be used as drug targets for the treatment of hypertension as well as for the prevention of all complications.

10       Peripheral vascular diseases are defined as vascular diseases in which arterial and/or venous flow is reduced resulting in an imbalance between blood supply and tissue oxygen demand. It includes chronic peripheral arterial occlusive disease (PAOD), acute arterial thrombosis and embolism, inflammatory vascular disorders, Raynaud's phenomenon, and venous disorders.

15       CNS disorders which may be treated include brain injuries, cerebrovascular diseases and their consequences, Parkinson's disease, corticobasal degeneration, motor neuron disease, dementia, including ALS, multiple sclerosis, traumatic brain injury, stroke, post-stroke, post-traumatic brain injury, and small-vessel cerebrovascular disease. Dementias, such as Alzheimer's disease, vascular dementia, dementia with Lewy  
20       bodies, frontotemporal dementia and Parkinsonism linked to chromosome 17, frontotemporal dementias, including Pick's disease, progressive nuclear palsy, corticobasal degeneration, Huntington's disease, thalamic degeneration, Creutzfeld-Jakob dementia, HIV dementia, schizophrenia with dementia, and Korsakoff's psychosis also can be treated. Similarly, it may be possible to treat cognitive-related  
25       disorders, such as mild cognitive impairment, age-associated memory impairment, age-related cognitive decline, vascular cognitive impairment, attention deficit disorders, attention deficit hyperactivity disorders, and memory disturbances in children with learning disabilities, by regulating the activity of human lysosomal acid lipase.

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- 54 -

Pain that is associated with CNS disorders also can be treated by regulating the activity of human lysosomal acid lipase. Pain which can be treated includes that associated with central nervous system disorders, such as multiple sclerosis, spinal cord injury, sciatica, failed back surgery syndrome, traumatic brain injury, epilepsy, Parkinson's disease, post-stroke, and vascular lesions in the brain and spinal cord (e.g., infarct, hemorrhage, vascular malformation). Non-central neuropathic pain includes that associated with post mastectomy pain, reflex sympathetic dystrophy (RSD), trigeminal neuralgioradioculopathy, post-surgical pain, HIV/AIDS related pain, cancer pain, metabolic neuropathies (e.g., diabetic neuropathy, vasculitic neuropathy secondary to connective tissue disease), paraneoplastic polyneuropathy associated, for example, with carcinoma of lung, or leukemia, or lymphoma, or carcinoma of prostate, colon or stomach, trigeminal neuralgia, cranial neuralgias, and post-herpetic neuralgia. Pain associated with cancer and cancer treatment also can be treated, as can headache pain (for example, migraine with aura, migraine without aura, and other migraine disorders), episodic and chronic tension-type headache, tension-type like headache, cluster headache, and chronic paroxysmal hemicrania.

This invention further pertains to the use of novel agents identified by the screening assays described above. Accordingly, it is within the scope of this invention to use a test compound identified as described herein in an appropriate animal model. For example, an agent identified as described herein (e.g., a modulating agent, an antisense nucleic acid molecule, a specific antibody, ribozyme, or a lysosomal acid lipase polypeptide binding molecule) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

A reagent which affects lysosomal acid lipase activity can be administered to a human cell, either *in vitro* or *in vivo*, to reduce lysosomal acid lipase activity. The

reagent preferably binds to an expression product of a human lysosomal acid lipase gene. If the expression product is a protein, the reagent is preferably an antibody. For treatment of human cells *ex vivo*, an antibody can be added to a preparation of stem cells which have been removed from the body. The cells can then be replaced  
5 in the same or another human body, with or without clonal propagation, as is known in the art.

In one embodiment, the reagent is delivered using a liposome. Preferably, the liposome is stable in the animal into which it has been administered for at least about  
10 30 minutes, more preferably for at least about 1 hour, and even more preferably for at least about 24 hours. A liposome comprises a lipid composition that is capable of targeting a reagent, particularly a polynucleotide, to a particular site in an animal, such as a human. Preferably, the lipid composition of the liposome is capable of targeting to a specific organ of an animal, such as the lung, liver, spleen, heart brain,  
15 lymph nodes, and skin.

A liposome useful in the present invention comprises a lipid composition that is capable of fusing with the plasma membrane of the targeted cell to deliver its contents to the cell. Preferably, the transfection efficiency of a liposome is about 0.5  
20  $\mu\text{g}$  of DNA per 16 nmole of liposome delivered to about  $10^6$  cells, more preferably about 1.0  $\mu\text{g}$  of DNA per 16 nmole of liposome delivered to about  $10^6$  cells, and even more preferably about 2.0  $\mu\text{g}$  of DNA per 16 nmol of liposome delivered to about  $10^6$  cells. Preferably, a liposome is between about 100 and 500 nm, more preferably between about 150 and 450 nm, and even more preferably between about 200 and  
25 400 nm in diameter.

Suitable liposomes for use in the present invention include those liposomes standardly used in, for example, gene delivery methods known to those of skill in the art. More preferred liposomes include liposomes having a polycationic lipid  
30 composition and/or liposomes having a cholesterol backbone conjugated to polyethylene glycol. Optionally, a liposome comprises a compound capable of



targeting the liposome to a particular cell type, such as a cell-specific ligand exposed on the outer surface of the liposome.

5       Complexing a liposome with a reagent such as an antisense oligonucleotide or ribozyme can be achieved using methods which are standard in the art (see, for example, U.S. Patent 5,705,151). Preferably, from about 0.1  $\mu$ g to about 10  $\mu$ g of polynucleotide is combined with about 8 nmol of liposomes, more preferably from about 0.5  $\mu$ g to about 5  $\mu$ g of polynucleotides are combined with about 8 nmol liposomes, and even more preferably about 1.0  $\mu$ g of polynucleotides is combined  
10       with about 8 nmol liposomes.

In another embodiment, antibodies can be delivered to specific tissues *in vivo* using receptor-mediated targeted delivery. Receptor-mediated DNA delivery techniques are taught in, for example, Findeis *et al.* *Trends in Biotechnol.* 11, 202-05 (1993);  
15       Chiou *et al.*, GENE THERAPEUTICS: METHODS AND APPLICATIONS OF DIRECT GENE TRANSFER (J.A. Wolff, ed.) (1994); Wu & Wu, *J. Biol. Chem.* 263, 621-24 (1988); Wu *et al.*, *J. Biol. Chem.* 269, 542-46 (1994); Zenke *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 87, 3655-59 (1990); Wu *et al.*, *J. Biol. Chem.* 266, 338-42 (1991).

#### 20       Determination of a Therapeutically Effective Dose

The determination of a therapeutically effective dose is well within the capability of those skilled in the art. A therapeutically effective dose refers to that amount of active ingredient which increases or decreases lysosomal acid lipase activity relative to the lysosomal acid lipase activity which occurs in the absence of the  
25       therapeutically effective dose.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models, usually mice, rabbits, dogs, or pigs. The animal model also can be used to determine the appropriate concentration range and  
30       route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

- 57 -

Therapeutic efficacy and toxicity, *e.g.*,  $ED_{50}$  (the dose therapeutically effective in 50% of the population) and  $LD_{50}$  (the dose lethal to 50% of the population), can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the ratio,  $LD_{50}/ED_{50}$ .

Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the  $ED_{50}$  with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active ingredient or to maintain the desired effect. Factors which can be taken into account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions can be administered every 3 to 4 days, every week, or once every two weeks depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts can vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

If the reagent is a single-chain antibody, polynucleotides encoding the antibody can be constructed and introduced into a cell either *ex vivo* or *in vivo* using well-established techniques including, but not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, "gene gun," and DEAE- or calcium phosphate-mediated transfection.

Effective *in vivo* dosages of an antibody are in the range of about 5 µg to about 50 µg/kg, about 50 µg to about 5 mg/kg, about 100 µg to about 500 µg/kg of patient body weight, and about 200 to about 250 µg/kg of patient body weight. For administration of polynucleotides encoding single-chain antibodies, effective *in vivo* dosages are in the range of about 100 ng to about 200 ng, 500 ng to about 50 mg, about 1 µg to about 2 mg, about 5 µg to about 500 µg, and about 20 µg to about 100 µg of DNA.

If the expression product is mRNA, the reagent is preferably an antisense oligonucleotide or a ribozyme. Polynucleotides which express antisense oligonucleotides or ribozymes can be introduced into cells by a variety of methods, as described above.

Preferably, a reagent reduces expression of a lysosomal acid lipase gene or the activity of a lysosomal acid lipase polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the reagent. The effectiveness of the mechanism chosen to decrease the level of expression of a lysosomal acid lipase gene or the activity of a lysosomal acid lipase polypeptide can be assessed using methods well known in the art, such as hybridization of nucleotide probes to lysosomal acid lipase-specific mRNA, quantitative RT-PCR, immunologic detection of a lysosomal acid lipase polypeptide, or measurement of lysosomal acid lipase activity.

In any of the embodiments described above, any of the pharmaceutical compositions of the invention can be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy can be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents can act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

10

Any of the therapeutic methods described above can be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

15

#### Diagnostic Methods

Human lysosomal acid lipase also can be used in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences which encode the enzyme. For example, differences can be determined between the cDNA or genomic sequence encoding lysosomal acid lipase in individuals afflicted with a disease and in normal individuals. If a mutation is observed in some or all of the afflicted individuals but not in normal individuals, then the mutation is likely to be the causative agent of the disease.

20

Sequence differences between a reference gene and a gene having mutations can be revealed by the direct DNA sequencing method. In addition, cloned DNA segments can be employed as probes to detect specific DNA segments. The sensitivity of this method is greatly enhanced when combined with PCR. For example, a sequencing primer can be used with a double-stranded PCR product or a single-stranded template molecule generated by a modified PCR. The sequence determination is performed

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- 60 -

by conventional procedures using radiolabeled nucleotides or by automatic sequencing procedures using fluorescent tags.

Genetic testing based on DNA sequence differences can be carried out by detection  
5 of alteration in electrophoretic mobility of DNA fragments in gels with or without  
denaturing agents. Small sequence deletions and insertions can be visualized, for  
example, by high resolution gel electrophoresis. DNA fragments of different  
sequences can be distinguished on denaturing formamide gradient gels in which the  
10 mobilities of different DNA fragments are retarded in the gel at different positions  
according to their specific melting or partial melting temperatures (*see, e.g., Myers et al., Science* 230, 1242, 1985). Sequence changes at specific locations can also be  
revealed by nuclease protection assays, such as RNase and S 1 protection or the  
chemical cleavage method (*e.g., Cotton et al., Proc. Natl. Acad. Sci. USA* 85,  
4397-4401, 1985). Thus, the detection of a specific DNA sequence can be performed  
15 by methods such as hybridization, RNase protection, chemical cleavage, direct DNA  
sequencing or the use of restriction enzymes and Southern blotting of genomic DNA.  
In addition to direct methods such as gel-electrophoresis and DNA sequencing,  
mutations can also be detected by *in situ* analysis.

20 Altered levels of a lysosomal acid lipase also can be detected in various tissues.  
Assays used to detect levels of the receptor polypeptides in a body sample, such as  
blood or a tissue biopsy, derived from a host are well known to those of skill in the  
art and include radioimmunoassays, competitive binding assays, Western blot  
analysis, and ELISA assays.

25 All patents and patent applications cited in this disclosure are expressly incorporated  
herein by reference. The above disclosure generally describes the present invention.  
A more complete understanding can be obtained by reference to the following  
specific examples which are provided for purposes of illustration only and are not  
30 intended to limit the scope of the invention.

**EXAMPLE 1***Detection of lysosomal acid lipase activity*

The polynucleotide of SEQ ID NO: 1 is inserted into the expression vector pCEV4 and the expression vector pCEV4-lysosomal acid lipase polypeptide obtained is transfected into human embryonic kidney 293 cells. From these cells extracts are obtained and lysosomal acid activity is determined in the following assay: a stock solution of 10 mg/ml *p*-nitrophenyl butyrate (PNPB, Sigma) is prepared in acetonitrile. The final concentration used the assay is 2 µg/ml. If optimization of the system is required, a range of PNPB concentrations is tested, from 0.25 µg/ml to 4 µg/ml. Two to ten µg of cell extract is incubated in 10 µg heparin (Sigma) and 0.1 M sodium phosphate, pH 7.2 (containing 0.9% NaCl); the reaction volume is 1 ml. Care is taken that the acetonitrile concentration is not above 1% v/v. Hydrolysis of PNPB results in an increase of absorbance at 400 nm. The reading is corrected for initial absorbance of PNPB. The reaction is stopped by addition of 3.25 ml methanol: chloroform: heptane (1: 0.9: 0.7) and shaking. Shirai and Jackson, *J. Biol. Chem.* 257, 1253-58, 1982. It is shown that the polypeptide of SEQ ID NO: 2 has a lysosomal acid lipase activity.

**EXAMPLE 2***Expression of recombinant human lysosomal acid lipase*

The *Pichia pastoris* expression vector pPICZB (Invitrogen, San Diego, CA) is used to produce large quantities of recombinant human lysosomal acid lipase polypeptides in yeast. The lysosomal acid lipase-encoding DNA sequence is derived from SEQ ID NO:1, 4, or 7. Before insertion into vector pPICZB, the DNA sequence is modified by well known methods in such a way that it contains at its 5'-end an initiation codon and at its 3'-end an enterokinase cleavage site, a His6 reporter tag and a termination codon. Moreover, at both termini recognition sequences for restriction endonucleases are added and after digestion of the multiple cloning site of pPICZ B with the corresponding restriction enzymes the modified DNA sequence is ligated into

- 62 -

pPICZB. This expression vector is designed for inducible expression in *Pichia pastoris*, driven by a yeast promoter. The resulting pPICZ/md-His6 vector is used to transform the yeast.

5 The yeast is cultivated under usual conditions in 5 liter shake flasks and the recombinantly produced protein isolated from the culture by affinity chromatography (Ni-NTA-Resin) in the presence of 8 M urea. The bound polypeptide is eluted with buffer, pH 3.5, and neutralized. Separation of the polypeptide from the His6 reporter tag is accomplished by site-specific proteolysis using enterokinase (Invitrogen, San  
10 Diego, CA) according to manufacturer's instructions. Purified human lysosomal acid lipase polypeptide is obtained.

### EXAMPLE 3

#### *Identification of test compounds that bind to lysosomal acid lipase polypeptides*

15 Purified lysosomal acid lipase polypeptides comprising a glutathione-S-transferase protein and absorbed onto glutathione-derivatized wells of 96-well microtiter plates are contacted with test compounds from a small molecule library at pH 7.0 in a physiological buffer solution. Human lysosomal acid lipase polypeptides comprise  
20 an amino acid sequence shown in SEQ ID NO:2, 5, or 6. The test compounds comprise a fluorescent tag. The samples are incubated for 5 minutes to one hour. Control samples are incubated in the absence of a test compound.

The buffer solution containing the test compounds is washed from the wells.  
25 Binding of a test compound to a lysosomal acid lipase polypeptide is detected by fluorescence measurements of the contents of the wells. A test compound which increases the fluorescence in a well by at least 15% relative to fluorescence of a well in which a test compound is not incubated is identified as a compound which binds to a lysosomal acid lipase polypeptide.

30

**EXAMPLE 4***Identification of a test compound which decreases lysosomal acid lipase gene expression*

- 5 A test compound is administered to a culture of human cells transfected with a lysosomal acid lipase expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the same type of cells which have not been transfected is incubated for the same time without the test compound to provide a negative control.
- 10 RNA is isolated from the two cultures as described in Chirgwin *et al.*, *Biochem. 18*, 5294-99, 1979). Northern blots are prepared using 20 to 30 µg total RNA and hybridized with a <sup>32</sup>P-labeled lysosomal acid lipase-specific probe at 65 °C in Express-hyb (CLONTECH). The probe comprises at least 11 contiguous nucleotides selected from the complement of SEQ ID NO:1, 4, or 7. A test compound which
- 15 decreases the lysosomal acid lipase-specific signal relative to the signal obtained in the absence of the test compound is identified as an inhibitor of lysosomal acid lipase gene expression.

**EXAMPLE 5**

- 20 *Identification of a test compound which decreases lysosomal acid lipase activity*

- A test compound is administered to a culture of human cells transfected with a lysosomal acid lipase expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the same type of cells which have not been transfected is
- 25 incubated for the same time without the test compound to provide a negative control.

*Lipase Activity Assay*

- A stock solution of 10 mg/ml *p*-nitrophenyl butyrate (PNPB, Sigma) is prepared in acetonitrile. The final concentration used the assay is 2 µg/ml. If optimization of the
- 30 system is required, a range of PNPB concentrations is tested, from 0.25 µg/ml to 4 µg/ml. Two to ten µg of a semicrude (partially purified) lipase fraction or 5 µg of



purified material is incubated in 10 µg heparin (Sigma) and 0.1 M sodium phosphate, pH 7.2 (containing 0.9% NaCl); the reaction volume is 1 ml. Care is taken that the acetonitrile concentration is not above 1% v/v.

- 5      Hydrolysis of PNPB results in an increase of absorbance at 400 nm. The reading is corrected for initial absorbance of PNPB. The reaction is stopped by addition of 3.25 ml methanol: chloroform: heptane (1: 0.9: 0.7) and shaking. Shirai and Jackson, *J. Biol. Chem.* 257, 1253-58, 1982.
- 10     A test compound which decreases the lipase activity of the lysosomal acid lipase relative to the lipase activity in the absence of the test compound is identified as an inhibitor of lysosomal acid lipase activity.

#### EXAMPLE 6

15      *Tissue-specific expression of lysosomal acid lipase*

The qualitative expression pattern of lysosomal acid lipase in various tissues is determined by Reverse Transcription-Polymerase Chain Reaction (RT-PCR). To demonstrate that lysosomal acid lipase is involved in cancer, expression is

20      determined in the following tissues: adrenal gland, bone marrow, brain, cerebellum, colon, fetal brain, fetal liver, heart, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thymus, thyroid, trachea, uterus, and peripheral blood lymphocytes. Expression in the following cancer cell lines also is determined: DU-

25      145 (prostate), NCI-H125 (lung), HT-29 (colon), COLO-205 (colon), A-549 (lung), NCI-H460 (lung), HT-116 (colon), DLD-1 (colon), MDA-MD-231 (breast), LS174T (colon), ZF-75 (breast), MDA-MN-435 (breast), HT-1080, MCF-7 (breast), and U87. Matched pairs of malignant and normal tissue from the same patient also are tested.

- 30      To demonstrate that lysosomal acid lipase is involved in the disease process of obesity, expression is determined in the following tissues: subcutaneous adipose

tissue, mesenteric adipose tissue, adrenal gland, bone marrow, brain (cerebellum, spinal cord, cerebral cortex, caudate, medulla, substantia nigra, and putamen), colon, fetal brain, heart, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testes, thymus, thyroid trachea, and uterus. Neuroblastoma cell lines SK-Nr-Be (2), Hr, Sk-N-As, HTB-10, IMR-32, SNSY-5Y, T3, SK-N-D2, D283, DAOY, CHP-2, U87MG, BE(2)C, T986, KANTS, MO59K, CHP234, C6 (rat), SK-N-F1, SK-PU-DW, PFSK-1, BE(2)M17, and MCIXC also are tested for lysosomal acid lipase expression. As a final step, the expression of lysosomal acid lipase in cells derived from normal individuals with the expression of cells derived from obese individuals is compared.

To demonstrate that lysosomal acid lipase is involved in the disease process of COPD, the initial expression panel consists of RNA samples from respiratory tissues and inflammatory cells relevant to COPD: lung (adult and fetal), trachea, freshly isolated alveolar type II cells, cultured human bronchial epithelial cells, cultured small airway epithelial cells, cultured bronchial smooth muscle cells, cultured H441 cells (Clara-like), freshly isolated neutrophils and monocytes, and cultured monocytes (macrophage-like). Body map profiling also is carried out, using total RNA panels purchased from Clontech. The tissues are adrenal gland, bone marrow, brain, colon, heart, kidney, liver, lung, mammary gland, pancreas, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testis, thymus, trachea, thyroid, and uterus.

To demonstrate that lysosomal acid lipase is involved in the disease process of diabetes, the following whole body panel is screened to show predominant or relatively high expression: subcutaneous and mesenteric adipose tissue, adrenal gland, bone marrow, brain, colon, fetal brain, heart, hypothalamus, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testis, thymus, thyroid, trachea, and uterus. Human islet cells and an islet cell library also are tested. As a final step, the expression of

lysosomal acid lipase in cells derived from normal individuals with the expression of cells derived from diabetic individuals is compared.

To demonstrate that lysosomal acid lipase is involved in CNS disorders, the following tissues are screened: fetal and adult brain, muscle, heart, lung, kidney, liver, thymus, testis, colon, placenta, trachea, pancreas, kidney, gastric mucosa, colon, liver, cerebellum, skin, cortex (Alzheimer's and normal), hypothalamus, cortex, amygdala, cerebellum, hippocampus, choroid, plexus, thalamus, and spinal cord.

*Quantitative expression profiling.* Quantitative expression profiling is performed by the form of quantitative PCR analysis called "kinetic analysis" firstly described in Higuchi *et al.*, *BioTechnology* 10, 413-17, 1992, and Higuchi *et al.*, *BioTechnology* 11, 1026-30, 1993. The principle is that at any given cycle within the exponential phase of PCR, the amount of product is proportional to the initial number of template copies.

If the amplification is performed in the presence of an internally quenched fluorescent oligonucleotide (TaqMan probe) complementary to the target sequence, the probe is cleaved by the 5'-3' endonuclease activity of Taq DNA polymerase and a fluorescent dye released in the medium (Holland *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 88, 7276-80, 1991). Because the fluorescence emission will increase in direct proportion to the amount of the specific amplified product, the exponential growth phase of PCR product can be detected and used to determine the initial template concentration (Heid *et al.*, *Genome Res.* 6, 986-94, 1996, and Gibson *et al.*, *Genome Res.* 6, 995-1001, 1996).

The amplification of an endogenous control can be performed to standardize the amount of sample RNA added to a reaction. In this kind of experiment, the control of choice is the 18S ribosomal RNA. Because reporter dyes with differing emission

- 67 -

spectra are available, the target and the endogenous control can be independently quantified in the same tube if probes labeled with different dyes are used.

All "real time PCR" measurements of fluorescence are made in the ABI Prism 7700.

5

*RNA extraction and cDNA preparation.* The total RNAs used for expression quantification are listed below along with their suppliers, if commercially available. RNAs labeled "from autopsy" are extracted from autoptic tissues with the TRIzol reagent (Life Technologies, MD) according to the manufacturer's protocol.

10

Fifty µg of each RNA are treated with DNase I for 1 hour at 37 °C in the following reaction mix: 0.2 U/µl RNase-free DNase I (Roche Diagnostics, Germany); 0.4 U/µl RNase inhibitor (PE Applied Biosystems, CA); 10 mM Tris-HCl pH 7.9; 10 mM MgCl<sub>2</sub>; 50 mM NaCl; and 1 mM DTT.

15

After incubation, RNA is extracted once with 1 volume of phenol:chloroform:isoamyl alcohol (24:24:1) and once with chloroform, and precipitated with 1/10 volume of 3 M NaAcetate, pH 5.2, and 2 volumes of ethanol.

20

Fifty µg of each RNA from the autoptic tissues are DNase treated with the DNA-free kit purchased from Ambion (Ambion, TX). After resuspension and spectrophotometric quantification, each sample is reverse transcribed with the TaqMan Reverse Transcription Reagents (PE Applied Biosystems, CA) according to the manufacturer's protocol. The final concentration of RNA in the reaction mix is 200 ng/µL. Reverse transcription is carried out with 2.5µM of random hexamer primers.

25

*TaqMan quantitative analysis.* Specific primers and probe are designed according to the recommendations of PE Applied Biosystems and are listed below:

30

forward primer: 5'-(gene specific sequence)-3'

reverse primer: 5'-(gene specific sequence)-3'

- 68 -

probe: 5'-(FAM)-(gene specific sequence)(TAMRA)-3'

where FAM = 6-carboxy-fluorescein

and TAMRA = 6-carboxy-tetramethyl-rhodamine.

5 The expected length of the PCR product is -(gene specific length)bp.

Quantification experiments are performed on 10 ng of reverse transcribed RNA from each sample. Each determination is done in triplicate.

10 Total cDNA content is normalized with the simultaneous quantification (multiplex PCR) of the 18S ribosomal RNA using the Pre-Developed TaqMan Assay Reagents (PDAR) Control Kit (PE Applied Biosystems, CA).

15 The assay reaction mix is as follows: 1X final TaqMan Universal PCR Master Mix (from 2X stock) (PE Applied Biosystems, CA); 1X PDAR control – 18S RNA (from 20X stock); 300 nM forward primer; 900 nM reverse primer; 200 nM probe; 10 ng cDNA; and water to 25 µl.

20 Each of the following steps are carried out once: pre PCR, 2 minutes at 50 °C, and 10 minutes at 95 °C. The following steps are carried out 40 times: denaturation, 15 seconds at 95 °C, annealing/extension, 1 minute at 60 °C.

25 The experiment is performed on an ABI Prism 7700 Sequence Detector (PE Applied Biosystems, CA). At the end of the run, fluorescence data acquired during PCR are processed as described in the ABI Prism 7700 user's manual in order to achieve better background subtraction as well as signal linearity with the starting target quantity.

**EXAMPLE 7***In vivo testing of compounds/target validation***1. Pain:****5     *Acute Pain***

Acute pain is measured on a hot plate mainly in rats. Two variants of hot plate testing are used: In the classical variant animals are put on a hot surface (52 to 56 °C) and the latency time is measured until the animals show nocifensive behavior, such as stepping or foot licking. The other variant is an increasing temperature hot plate  
10     where the experimental animals are put on a surface of neutral temperature. Subsequently this surface is slowly but constantly heated until the animals begin to lick a hind paw. The temperature which is reached when hind paw licking begins is a measure for pain threshold.

15     Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

***Persistent Pain***

20     Persistent pain is measured with the formalin or capsaicin test, mainly in rats. A solution of 1 to 5% formalin or 10 to 100 µg capsaicin is injected into one hind paw of the experimental animal. After formalin or capsaicin application the animals show nocifensive reactions like flinching, licking and biting of the affected paw. The number of nocifensive reactions within a time frame of up to 90 minutes is a measure  
25     for intensity of pain.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to formalin or capsaicin administration.

### *Neuropathic Pain*

Neuropathic pain is induced by different variants of unilateral sciatic nerve injury mainly in rats. The operation is performed under anesthesia. The first variant of sciatic nerve injury is produced by placing loosely constrictive ligatures around the  
5 common sciatic nerve. The second variant is the tight ligation of about the half of the diameter of the common sciatic nerve. In the next variant, a group of models is used in which tight ligations or transections are made of either the L5 and L6 spinal nerves, or the L<sub>4</sub> spinal nerve only. The fourth variant involves an axotomy of two  
10 of the three terminal branches of the sciatic nerve (tibial and common peroneal nerves) leaving the remaining sural nerve intact whereas the last variant comprises the axotomy of only the tibial branch leaving the sural and common nerves uninjured. Control animals are treated with a sham operation.

Postoperatively, the nerve injured animals develop a chronic mechanical allodynia,  
15 cold allodynia, as well as a thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA; Electronic von Frey System, Somedic Sales AB, Hörby, Sweden). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy), or by  
20 means of a cold plate of 5 to 10 °C where the nocifensive reactions of the affected hind paw are counted as a measure of pain intensity. A further test for cold induced pain is the counting of nocifensive reactions, or duration of nocifensive responses after plantar administration of acetone to the affected hind limb. Chronic pain in general is assessed by registering the circadian rhythms in activity (Surjo and  
25 Arndt, Universität zu Köln, Cologne, Germany), and by scoring differences in gait (foot print patterns; FOOTPRINTS program, Klapdor et al., 1997. A low cost method to analyze footprint patterns. J. Neurosci. Methods 75, 49-54).

Compounds are tested against sham operated and vehicle treated control groups.  
30 Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

***Inflammatory Pain***

Inflammatory pain is induced mainly in rats by injection of 0.75 mg carrageenan or complete Freund's adjuvant into one hind paw. The animals develop an edema with mechanical allodynia as well as thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy, Paw thermal stimulator, G. Ozaki, University of California, USA). For edema measurement two methods are being used. In the first method, the animals are sacrificed and the affected hindpaws sectioned and weighed. The second method comprises differences in paw volume by measuring water displacement in a plethysmometer (Ugo Basile, Comerio, Italy).

Compounds are tested against uninflamed as well as vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

***Diabetic Neuropathic Pain***

Rats treated with a single intraperitoneal injection of 50 to 80 mg/kg streptozotocin develop a profound hyperglycemia and mechanical allodynia within 1 to 3 weeks. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA).

Compounds are tested against diabetic and non-diabetic vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.



## 2. Parkinson's disease

### *6-Hydroxydopamine (6-OH-DA) Lesion*

Degeneration of the dopaminergic nigrostriatal and striatopallidal pathways is the central pathological event in Parkinson's disease. This disorder has been mimicked experimentally in rats using single/sequential unilateral stereotaxic injections of 6-OH-DA into the medium forebrain bundle (MFB).

Male Wistar rats (Harlan Winkelmann, Germany), weighing  $200 \pm 250$  g at the beginning of the experiment, are used. The rats are maintained in a temperature- and humidity-controlled environment under a 12 h light/dark cycle with free access to food and water when not in experimental sessions. The following in vivo protocols are approved by the governmental authorities. All efforts are made to minimize animal suffering, to reduce the number of animals used, and to utilize alternatives to in vivo techniques.

Animals are administered pargyline on the day of surgery (Sigma, St. Louis, MO, USA; 50 mg/kg i.p.) in order to inhibit metabolism of 6-OHDA by monoamine oxidase and desmethylinipramine HCl (Sigma; 25 mg/kg i.p.) in order to prevent uptake of 6-OHDA by noradrenergic terminals. Thirty minutes later the rats are anesthetized with sodium pentobarbital (50 mg/kg) and placed in a stereotaxic frame. In order to lesion the DA nigrostriatal pathway 4  $\mu$ l of 0.01% ascorbic acid-saline containing 8  $\mu$ g of 6-OHDA HBr (Sigma) are injected into the left medial fore-brain bundle at a rate of 1  $\mu$ l/min (2.4 mm anterior, 1.49 mm lateral, -2.7 mm ventral to Bregma and the skull surface). The needle is left in place an additional 5 min to allow diffusion to occur.

### Stepping Test

Forelimb akinesia is assessed three weeks following lesion placement using a modified stepping test protocol. In brief, the animals are held by the experimenter with one hand fixing the hindlimbs and slightly raising the hind part above the surface. One paw is touching the table, and is then moved slowly sideways (5 s for 1

m), first in the forehand and then in the backhand direction. The number of adjusting steps is counted for both paws in the backhand and forehand direction of movement. The sequence of testing is right paw forehand and backhand adjusting stepping, followed by left paw forehand and backhand directions. The test is repeated three times on three consecutive days, after an initial training period of three days prior to the first testing. Forehand adjusted stepping reveals no consistent differences between lesioned and healthy control animals. Analysis is therefore restricted to backhand adjusted stepping.

#### 10 Balance Test

Balance adjustments following postural challenge are also measured during the stepping test sessions. The rats are held in the same position as described in the stepping test and, instead of being moved sideways, tilted by the experimenter towards the side of the paw touching the table. This maneuver results in loss of balance and the ability of the rats to regain balance by forelimb movements is scored on a scale ranging from 0 to 3. Score 0 is given for a normal forelimb placement. When the forelimb movement is delayed but recovery of postural balance detected, score 1 is given. Score 2 represents a clear, yet insufficient, forelimb reaction, as evidenced by muscle contraction, but lack of success in recovering balance, and score 3 is given for no reaction of movement. The test is repeated three times a day on each side for three consecutive days after an initial training period of three days prior to the first testing.

#### Staircase Test (Paw Reaching)

A modified version of the staircase test is used for evaluation of paw reaching behavior three weeks following primary and secondary lesion placement. Plexiglass test boxes with a central platform and a removable staircase on each side are used. The apparatus is designed such that only the paw on the same side at each staircase can be used, thus providing a measure of independent forelimb use. For each test the animals are left in the test boxes for 15 min. The double staircase is filled with 7 x 3 chow pellets (Precision food pellets, formula: P, purified rodent diet, size 45 mg;

Sandown Scientific) on each side. After each test the number of pellets eaten (successfully retrieved pellets) and the number of pellets taken (touched but dropped) for each paw and the success rate (pellets eaten/pellets taken) are counted separately. After three days of food deprivation (12 g per animal per day) the animals are tested for 11 days. Full analysis is conducted only for the last five days.

### ***MPTP treatment***

The neurotoxin 1-methyl-4-phenyl-1,2,3,6-tetrahydro-pyridine (MPTP) causes degeneration of mesencephalic dopaminergic (DAergic) neurons in rodents, non-human primates, and humans and, in so doing, reproduces many of the symptoms of Parkinson's disease. MPTP leads to a marked decrease in the levels of dopamine and its metabolites, and in the number of dopaminergic terminals in the striatum as well as severe loss of the tyrosine hydroxylase (TH)-immunoreactive cell bodies in the substantia nigra, pars compacta.

In order to obtain severe and long-lasting lesions, and to reduce mortality, animals receive single injections of MPTP, and are then tested for severity of lesion 7–10 days later. Successive MPTP injections are administered on days 1, 2 and 3. Animals receive application of 4 mg/kg MPTP hydrochloride (Sigma) in saline once daily. All injections are intraperitoneal (i.p.) and the MPTP stock solution is frozen between injections. Animals are decapitated on day 11.

### **Immunohistology**

At the completion of behavioral experiments, all animals are anaesthetized with 3 ml thiopental (1 g/40 ml i.p., Tyrol Pharma). The mice are perfused transcardially with 0.01 M PBS (pH 7.4) for 2 min, followed by 4% paraformaldehyde (Merck) in PBS for 15 min. The brains are removed and placed in 4% paraformaldehyde for 24 h at 4 °C. For dehydration they are then transferred to a 20% sucrose (Merck) solution in 0.1 M PBS at 4 °C until they sink. The brains are frozen in methylbutane at -20 °C for 2 min and stored at -70 °C. Using a sledge microtome (mod. 3800-Frigocut, Leica), 25 µm sections are taken from the genu of the corpus callosum (AP 1.7 mm) to the

hippocampus (AP 21.8 mm) and from AP 24.16 to AP 26.72. Forty-six sections are cut and stored in assorters in 0.25 M Tris buffer (pH 7.4) for immunohistochemistry.

5 A series of sections is processed for free-floating tyrosine hydroxylase (TH) immunohistochemistry. Following three rinses in 0.1 M PBS, endogenous peroxidase activity is quenched for 10 min in 0.3% H<sub>2</sub>O<sub>2</sub> ±PBS. After rinsing in PBS, sections are preincubated in 10% normal bovine serum (Sigma) for 5 min as blocking agent and transferred to either primary anti-rat TH rabbit antiserum (dilution 1:2000).

10 Following overnight incubation at room temperature, sections for TH immunoreactivity are rinsed in PBS (2 x10 min) and incubated in biotinylated anti-rabbit immunoglobulin G raised in goat (dilution 1:200) (Vector) for 90 min, rinsed repeatedly and transferred to Vectastain ABC (Vector) solution for 1 h. 3,3'-  
15 -Diaminobenzidine tetrahydrochloride (DAB; Sigma) in 0.1 M PBS, supplemented with 0.005% H<sub>2</sub>O<sub>2</sub>, serves as chromogen in the subsequent visualization reaction. Sections are mounted on to gelatin-coated slides, left to dry overnight, counter-stained with hematoxylin dehydrated in ascending alcohol concentrations and cleared in butylacetate. Coverslips are mounted on entellan.

#### 20 Rotarod Test

We use a modification of the procedure described by Rozas and Labandeira-Garcia (1997), with a CR-1 Rotamex system (Columbus Instruments, Columbus, OH) comprising an IBM-compatible personal computer, a CIO-24 data acquisition card, a  
25 control unit, and a four-lane rotarod unit. The rotarod unit consists of a rotating spindle (diameter 7.3 cm) and individual compartments for each mouse. The system software allows preprogramming of session protocols with varying rotational speeds (0-80 rpm). Infrared beams are used to detect when a mouse has fallen onto the base grid beneath the rotarod. The system logs the fall as the end of the experiment for  
30 that mouse, and the total time on the rotarod, as well as the time of the fall and all the

set-up parameters, are recorded. The system also allows a weak current to be passed through the base grid, to aid training.

### 3. Dementia

#### 5     *The object recognition task*

The object recognition task has been designed to assess the effects of experimental manipulations on the cognitive performance of rodents. A rat is placed in an open field, in which two identical objects are present. The rats inspects both objects during the first trial of the object recognition task. In a second trial, after a retention interval of for example 24 hours, one of the two objects used in the first trial, the 'familiar' object, and a novel object are placed in the open field. The inspection time at each of the objects is registered. The basic measures in the OR task is the time spent by a rat exploring the two object the second trial. Good retention is reflected by higher exploration times towards the novel than the 'familiar' object.

15

Administration of the putative cognition enhancer prior to the first trial predominantly allows assessment of the effects on acquisition, and eventually on consolidation processes. Administration of the testing compound after the first trial allows to assess the effects on consolidation processes, whereas administration before the second trial allows to measure effects on retrieval processes.

20

#### *The passive avoidance task*

The passive avoidance task assesses memory performance in rats and mice. The inhibitory avoidance apparatus consists of a two-compartment box with a light compartment and a dark compartment. The two compartments are separated by a guillotine door that can be operated by the experimenter. A threshold of 2 cm separates the two compartments when the guillotine door is raised. When the door is open, the illumination in the dark compartment is about 2 lux. The light intensity is about 500 lux at the center of the floor of the light compartment.

25

30

Two habituation sessions, one shock session, and a retention session are given, separated by inter-session intervals of 24 hours. In the habituation sessions and the retention session the rat is allowed to explore the apparatus for 300 sec. The rat is placed in the light compartment, facing the wall opposite to the guillotine door. After  
5 an accommodation period of 15 sec. the guillotine door is opened so that all parts of the apparatus can be visited freely. Rats normally avoid brightly lit areas and will enter the dark compartment within a few seconds.

10 In the shock session the guillotine door between the compartments is lowered as soon as the rat has entered the dark compartment with its four paws, and a scrambled 1 mA footshock is administered for 2 sec. The rat is removed from the apparatus and put back into its home cage. The procedure during the retention session is identical to that of the habituation sessions.

15 The step-through latency, that is the first latency of entering the dark compartment (in sec.) during the retention session is an index of the memory performance of the animal; the longer the latency to enter the dark compartment, the better the retention is. A testing compound is given half an hour before the shock session, together with  
20 1 mg\*kg<sup>-1</sup> scopolamine. Scopolamine impairs the memory performance during the retention session 24 hours later. If the test compound increases the enter latency compared with the scopolamine-treated controls, is likely to possess cognition enhancing potential.

#### *The Morris water escape task*

25 The Morris water escape task measures spatial orientation learning in rodents. It is a test system that has extensively been used to investigate the effects of putative therapeutic on the cognitive functions of rats and mice. The performance of an animal is assessed in a circular water tank with an escape platform that is submerged about 1 cm below the surface of the water. The escape platform is not visible for an  
30 animal swimming in the water tank. Abundant extra-maze cues are provided by the

furniture in the room, including desks, computer equipment, a second water tank, the presence of the experimenter, and by a radio on a shelf that is playing softly.

5 The animals receive four trials during five daily acquisition sessions. A trial is started by placing an animal into the pool, facing the wall of the tank. Each of four starting positions in the quadrants north, east, south, and west is used once in a series of four trials; their order is randomized. The escape platform is always in the same position. A trial is terminated as soon as the animal had climbs onto the escape platform or when 90 seconds have elapsed, whichever event occurs first. The animal is allowed  
10 to stay on the platform for 30 seconds. Then it is taken from the platform and the next trial is started. If an animal did not find the platform within 90 seconds it is put on the platform by the experimenter and is allowed to stay there for 30 seconds. After the fourth trial of the fifth daily session, an additional trial is given as a probe trial: the platform is removed, and the time the animal spends in the four quadrants is  
15 measured for 30 or 60 seconds. In the probe trial, all animals start from the same start position, opposite to the quadrant where the escape platform had been positioned during acquisition.

Four different measures are taken to evaluate the performance of an animal during  
20 acquisition training: escape latency, traveled distance, distance to platform, and swimming speed. The following measures are evaluated for the probe trial: time (s) in quadrants and traveled distance (cm) in the four quadrants. The probe trial provides additional information about how well an animal learned the position of the escape platform. If an animal spends more time and swims a longer distance in the  
25 quadrant where the platform had been positioned during the acquisition sessions than in any other quadrant, one concludes that the platform position has been learned well.

In order to assess the effects of putative cognition enhancing compounds, rats or mice with specific brain lesions which impair cognitive functions, or animals treated  
30 with compounds such as scopolamine or MK-801, which interfere with normal learning, or aged animals which suffer from cognitive deficits, are used.

*The T-maze spontaneous alternation task*

The T-maze spontaneous alternation task (TeMCAT) assesses the spatial memory performance in mice. The start arm and the two goal arms of the T-maze are provided with guillotine doors which can be operated manually by the experimenter. 5 A mouse is put into the start arm at the beginning of training. The guillotine door is closed. In the first trial, the 'forced trial', either the left or right goal arm is blocked by lowering the guillotine door. After the mouse has been released from the start arm, it will negotiate the maze, eventually enter the open goal arm, and return to the start position, where it will be confined for 5 seconds, by lowering the guillotine 10 door. Then, the animal can choose freely between the left and right goal arm (all guillotine-doors opened) during 14 'free choice' trials. As soon the mouse has entered one goal arm, the other one is closed. The mouse eventually returns to the start arm and is free to visit whichever goal arm it wants after having been confined 15 to the start arm for 5 seconds. After completion of 14 free choice trials in one session, the animal is removed from the maze. During training, the animal is never handled.

The per-cent alternations out of 14 trials is calculated. This percentage and the total 20 time needed to complete the first forced trial and the subsequent 14 free choice trials (in s) is analyzed. Cognitive deficits are usually induced by an injection of scopolamine, 30 min before the start of the training session. Scopolamine reduced the per-cent alternations to chance level, or below. A cognition enhancer, which is always administered before the training session, will at least partially, antagonize the 25 scopolamine-induced reduction in the spontaneous alternation rate.



**EXAMPLE 8***Diabetes: In vivo testing of compounds/target validation*

## 1. Glucose Production:

5 Over-production of glucose by the liver, due to an enhanced rate of gluconeogenesis, is the major cause of fasting hyperglycemia in diabetes. Overnight fasted normal rats or mice have elevated rates of gluconeogenesis as do streptozotocin-induced diabetic rats or mice fed ad libitum. Rats are made diabetic with a single intravenous injection of 40 mg/kg of streptozotocin while C57BL/KsJ mice are given 40-60 mg/kg i.p. for 5  
10 consecutive days. Blood glucose is measured from tail-tip blood and then compounds are administered via different routes (p.o., i.p., i.v., s.c.). Blood is collected at various times thereafter and glucose measured. Alternatively, compounds are administered for several days, then the animals are fasted  
15 overnight, blood is collected and plasma glucose measured. Compounds that inhibit glucose production will decrease plasma glucose levels compared to the vehicle-treated control group.

## 2. Insulin Sensitivity:

20 Both ob/ob and db/db mice as well as diabetic Zucker rats are hyperglycemic, hyperinsulinemic and insulin resistant. The animals are pre-bled, their glucose levels measured, and then they are grouped so that the mean glucose level is the same for each group. Compounds are administered daily either q.d. or b.i.d. by different routes (p.o., i.p., s.c.) for 7-28 days. Blood is collected at  
25 various times and plasma glucose and insulin levels determined. Compounds that improve insulin sensitivity in these models will decrease both plasma glucose and insulin levels when compared to the vehicle-treated control group.^

### 3. Insulin Secretion:

Compounds that enhance insulin secretion from the pancreas will increase plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin levels, compounds are administered by different routes (p.o., i.p., s.c. or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60 and 90 minutes and plasma glucose levels determined. Compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

Compounds that enhance insulin secretion from the pancreas will increase plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin levels, test compounds which regulate lysosomal acid lipase are administered by different routes (p.o., i.p., s.c., or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Test compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60, and 90 minutes and plasma glucose levels determined. Test compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

4. Glucose Production:

Over-production of glucose by the liver, due to an enhanced rate of gluconeogenesis, is the major cause of fasting hyperglycemia in diabetes.

5 Overnight fasted normal rats or mice have elevated rates of gluconeogenesis as do streptozotocin-induced diabetic rats or mice fed ad libitum. Rats are made diabetic with a single intravenous injection of 40 mg/kg of streptozotocin while C57BL/KsJ mice are given 40-60 mg/kg i.p. for 5 consecutive days. Blood glucose is measured from tail-tip blood and then

10 compounds are administered via different routes (p.o., i.p., i.v., s.c.). Blood is collected at various times thereafter and glucose measured. Alternatively, compounds are administered for several days, then the animals are fasted overnight, blood is collected and plasma glucose measured. Compounds that inhibit glucose production will decrease plasma glucose levels compared to

15 the vehicle-treated control group.

5. Insulin Sensitivity:

Both ob/ob and db/db mice as well as diabetic Zucker rats are hyperglycemic, hyperinsulinemic and insulin resistant. The animals are pre-bled, their glucose

20 levels measured, and then they are grouped so that the mean glucose level is the same for each group. Compounds are administered daily either q.d. or b.i.d. by different routes (p.o., i.p., s.c.) for 7-28 days. Blood is collected at various times and plasma glucose and insulin levels determined. Compounds that improve insulin sensitivity in these models will decrease both plasma

25 glucose and insulin levels when compared to the vehicle-treated control group.

6. Insulin Secretion:

Compounds that enhance insulin secretion from the pancreas will increase

30 plasma insulin levels and improve the disappearance of plasma glucose following the administration of a glucose load. When measuring insulin

levels, compounds are administered by different routes (p.o., i.p., s.c. or i.v.) to overnight fasted normal rats or mice. At the appropriate time an intravenous glucose load (0.4g/kg) is given, blood is collected one minute later. Plasma insulin levels are determined. Compounds that enhance insulin secretion will increase plasma insulin levels compared to animals given only glucose. When measuring glucose disappearance, animals are bled at the appropriate time after compound administration, then given either an oral or intraperitoneal glucose load (1g/kg), bled again after 15, 30, 60 and 90 minutes and plasma glucose levels determined. Compounds that increase insulin levels will decrease glucose levels and the area-under-the glucose curve when compared to the vehicle-treated group given only glucose.

## **EXAMPLE 9**

### ***In vivo testing of compounds/target validation***

#### **1. Acute Mechanistic Assays**

##### ***1.1. Reduction in Mitogenic Plasma Hormone Levels***

This non-tumor assay measures the ability of a compound to reduce either the endogenous level of a circulating hormone or the level of hormone produced in response to a biologic stimulus. Rodents are administered test compound (p.o., i.p., i.v., i.m., or s.c.). At a predetermined time after administration of test compound, blood plasma is collected. Plasma is assayed for levels of the hormone of interest. If the normal circulating levels of the hormone are too low and/or variable to provide consistent results, the level of the hormone may be elevated by a pre-treatment with a biologic stimulus (i.e., LHRH may be injected i.m. into mice at a dosage of 30 ng/mouse to induce a burst of testosterone synthesis). The timing of plasma collection would be adjusted to coincide with the peak of the induced hormone response. Compound effects are compared to a vehicle-treated control group. An F-test is performed to determine if the variance is equal or unequal followed by a Student's t-test. Significance is p value  $\leq 0.05$  compared to the vehicle control group.

### 1.2. *Hollow Fiber Mechanism of Action Assay*

Hollow fibers are prepared with desired cell line(s) and implanted intraperitoneally and/or subcutaneously in rodents. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Fibers are harvested in accordance with specific readout assay protocol, these may include assays for gene expression (bDNA, PCR, or Taqman), or a specific biochemical activity (i.e., cAMP levels. Results are analyzed by Student's t-test or Rank Sum test after the variance between groups is compared by an F-test, with significance at  $p \leq 0.05$  as compared to the vehicle control group.

## 2. *Subacute Functional In Vivo Assays*

### 2.1. *Reduction in Mass of Hormone Dependent Tissues*

This is another non-tumor assay that measures the ability of a compound to reduce the mass of a hormone dependent tissue (i.e., seminal vesicles in males and uteri in females). Rodents are administered test compound (p.o., i.p., i.v., i.m., or s.c.) according to a predetermined schedule and for a predetermined duration (i.e., 1 week). At termination of the study, animals are weighed, the target organ is excised, any fluid is expressed, and the weight of the organ is recorded. Blood plasma may also be collected. Plasma may be assayed for levels of a hormone of interest or for levels of test agent. Organ weights may be directly compared or they may be normalized for the body weight of the animal. Compound effects are compared to a vehicle-treated control group. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test. Significance is  $p \text{ value} \leq 0.05$  compared to the vehicle control group.

### 2.2. *Hollow Fiber Proliferation Assay*

Hollow fibers are prepared with desired cell line(s) and implanted intraperitoneally and/or subcutaneously in rodents. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Fibers are harvested in accordance

with specific readout assay protocol. Cell proliferation is determined by measuring a marker of cell number (i.e., MTT or LDH). The cell number and change in cell number from the starting inoculum are analyzed by Student's t-test or Rank Sum test after the variance between groups is compared by an F-test, with significance at  $p \leq 0.05$  as compared to the vehicle control group.

### 2.3. *Anti-angiogenesis Models*

#### 2.3.1. *Corneal Angiogenesis*

Hydron pellets with or without growth factors or cells are implanted into a micropocket surgically created in the rodent cornea. Compound administration may be systemic or local (compound mixed with growth factors in the hydron pellet). Corneas are harvested at 7 days post implantation immediately following intracardiac infusion of colloidal carbon and are fixed in 10% formalin. Readout is qualitative scoring and/or image analysis. Qualitative scores are compared by Rank Sum test. Image analysis data is evaluated by measuring the area of neovascularization (in pixels) and group averages are compared by Student's t-test (2 tail). Significance is  $p \leq 0.05$  as compared to the growth factor or cells only group.

#### 2.3.2. *Matrigel Angiogenesis*

Matrigel, containing cells or growth factors, is injected subcutaneously. Compounds are administered p.o., i.p., i.v., i.m., or s.c. Matrigel plugs are harvested at predetermined time point(s) and prepared for readout. Readout is an ELISA-based assay for hemoglobin concentration and/or histological examination (i.e. vessel count, special staining for endothelial surface markers: CD31, factor-8). Readouts are analyzed by Student's t-test, after the variance between groups is compared by an F-test, with significance determined at  $p \leq 0.05$  as compared to the vehicle control group.

### 3. Primary Antitumor Efficacy

#### 3.1. Early Therapy Models

##### 3.1.1. Subcutaneous Tumor

Tumor cells or fragments are implanted subcutaneously on Day 0. Vehicle and/or compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule starting at a time, usually on Day 1, prior to the ability to measure the tumor burden. Body weights and tumor measurements are recorded 2-3 times weekly. Mean net body and tumor weights are calculated for each data collection day. Anti-tumor efficacy may be initially determined by comparing the size of treated (T) and control (C) tumors on a given day by a Student's t-test, after the variance between groups is compared by an F-test, with significance determined at  $p \leq 0.05$ . The experiment may also be continued past the end of dosing in which case tumor measurements would continue to be recorded to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is  $p \leq 0.05$ .

##### 3.1.2. Intraperitoneal/Intracranial Tumor Models

Tumor cells are injected intraperitoneally or intracranially on Day 0. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule starting on Day 1. Observations of morbidity and/or mortality are recorded twice daily. Body weights are measured and recorded twice weekly. Morbidity/mortality data is expressed in terms of the median time of survival and the number of long-term survivors is indicated separately. Survival times are used to generate Kaplan-Meier curves. Significance is  $p \leq 0.05$  by a log-rank test compared to the control group in the experiment.

### 3.2. *Established Disease Model*

Tumor cells or fragments are implanted subcutaneously and grown to the desired size for treatment to begin. Once at the predetermined size range, mice are randomized into treatment groups. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Tumor and body weights are measured and recorded 2-3 times weekly. Mean tumor weights of all groups over days post inoculation are graphed for comparison. An F-test is performed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is  $p \leq 0.05$  as compared to the control group. Tumor measurements may be recorded after dosing has stopped to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is  $p \text{ value} \leq 0.05$  compared to the vehicle control group.

### 3.3. *Orthotopic Disease Models*

#### 3.3.1. *Mammary Fat Pad Assay*

Tumor cells or fragments, of mammary adenocarcinoma origin, are implanted directly into a surgically exposed and reflected mammary fat pad in rodents. The fat pad is placed back in its original position and the surgical site is closed. Hormones may also be administered to the rodents to support the growth of the tumors. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Tumor and body weights are measured and recorded 2-3 times weekly. Mean tumor weights of all groups over days post inoculation are graphed for comparison. An F-test is performed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is  $p \leq 0.05$  as compared to the control group.



Tumor measurements may be recorded after dosing has stopped to monitor tumor growth delay. Tumor growth delays are expressed as the difference in the median time for the treated and control groups to attain a predetermined size divided by the median time for the control group to attain that size. Growth delays are compared by generating Kaplan-Meier curves from the times for individual tumors to attain the evaluation size. Significance is  $p \text{ value} \leq 0.05$  compared to the vehicle control group. In addition, this model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ, or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at  $p \leq 0.05$  compared to the control group in the experiment.

### 3.3.2. *Intraprostatic Assay*

Tumor cells or fragments, of prostatic adenocarcinoma origin, are implanted directly into a surgically exposed dorsal lobe of the prostate in rodents. The prostate is externalized through an abdominal incision so that the tumor can be implanted specifically in the dorsal lobe while verifying that the implant does not enter the seminal vesicles. The successfully inoculated prostate is replaced in the abdomen and the incisions through the abdomen and skin are closed. Hormones may also be administered to the rodents to support the growth of the tumors. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is

$p \leq 0.05$  as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the lungs), or measuring the target organ weight (i.e., the regional lymph nodes). The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at  $p \leq 0.05$  compared to the control group in the experiment.

### 10 3.3.3. *Intrabronchial Assay*

Tumor cells of pulmonary origin may be implanted intrabronchially by making an incision through the skin and exposing the trachea. The trachea is pierced with the beveled end of a 25 gauge needle and the tumor cells are inoculated into the main bronchus using a flat-ended 27 gauge needle with a 90° bend. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope.

20 An F-test is preformed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is  $p \leq 0.05$  as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at

25 termination of the study by counting the number of visible foci per target organ (i.e., the contralateral lung), or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at  $p \leq 0.05$  compared to the control group in the experiment.

### 3.3.4. *Intracecal Assay*

Tumor cells of gastrointestinal origin may be implanted intracurally by making an abdominal incision through the skin and externalizing the intestine. Tumor cells are inoculated into the cecal wall without penetrating the lumen of the intestine using a 27 or 30 gauge needle. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Body weights are measured and recorded 2-3 times weekly. At a predetermined time, the experiment is terminated and the animal is dissected. The size of the primary tumor is measured in three dimensions using either a caliper or an ocular micrometer attached to a dissecting scope. An F-test is performed to determine if the variance is equal or unequal followed by a Student's t-test to compare tumor sizes in the treated and control groups at the end of treatment. Significance is  $p \leq 0.05$  as compared to the control group. This model provides an opportunity to increase the rate of spontaneous metastasis of this type of tumor. Metastasis can be assessed at termination of the study by counting the number of visible foci per target organ (i.e., the liver), or measuring the target organ weight. The means of these endpoints are compared by Student's t-test after conducting an F-test, with significance determined at  $p \leq 0.05$  compared to the control group in the experiment.

## 4. **Secondary (Metastatic) Antitumor Efficacy**

### 4.1. *Spontaneous Metastasis*

Tumor cells are inoculated s.c. and the tumors allowed to grow to a predetermined range for spontaneous metastasis studies to the lung or liver. These primary tumors are then excised. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule which may include the period leading up to the excision of the primary tumor to evaluate therapies directed at inhibiting the early stages of tumor metastasis. Observations of morbidity and/or mortality are recorded daily. Body weights are measured and recorded twice weekly. Potential endpoints include survival time, numbers of visible foci per target organ, or target organ weight.

- 91 -

When survival time is used as the endpoint the other values are not determined. Survival data is used to generate Kaplan-Meier curves. Significance is  $p \leq 0.05$  by a log-rank test compared to the control group in the experiment. The mean number of visible tumor foci, as determined under a dissecting microscope, and the mean target organ weights are compared by Student's t-test after conducting an F-test, with significance determined at  $p \leq 0.05$  compared to the control group in the experiment for both of these endpoints.

#### 4.2. *Forced Metastasis*

Tumor cells are injected into the tail vein, portal vein, or the left ventricle of the heart in experimental (forced) lung, liver, and bone metastasis studies, respectively. Compounds are administered p.o., i.p., i.v., i.m., or s.c. according to a predetermined schedule. Observations of morbidity and/or mortality are recorded daily. Body weights are measured and recorded twice weekly. Potential endpoints include survival time, numbers of visible foci per target organ, or target organ weight. When survival time is used as the endpoint the other values are not determined. Survival data is used to generate Kaplan-Meier curves. Significance is  $p \leq 0.05$  by a log-rank test compared to the control group in the experiment. The mean number of visible tumor foci, as determined under a dissecting microscope, and the mean target organ weights are compared by Student's t-test after conducting an F-test, with significance at  $p \leq 0.05$  compared to the vehicle control group in the experiment for both endpoints.

**CLAIMS**

1. An isolated polynucleotide encoding a lysosomal acid lipase polypeptide and being selected from the group consisting of:

5

- a) a polynucleotide encoding a lysosomal acid lipase polypeptide comprising an amino acid sequence selected from the group consisting of:

10

amino acid sequences which are at least about 54% identical to

the amino acid sequence shown in SEQ ID NO: 2;

the amino acid sequence shown in SEQ ID NO: 2;

amino acid sequences which are at least about 54% identical to

the amino acid sequence shown in SEQ ID NO: 5;

the amino acid sequence shown in SEQ ID NO: 5;

15

amino acid sequences which are at least about 54% identical to

the amino acid sequence shown in SEQ ID NO: 6; and

the amino acid sequence shown in SEQ ID NO: 6.

20

- b) a polynucleotide comprising the sequence of SEQ ID NO: 1, 4 or 7;

- c) a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b);

25

- d) a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code; and

30

- e) a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d).

2. An expression vector containing any polynucleotide of claim 1.

3. A host cell containing the expression vector of claim 2.
4. A substantially purified lysosomal acid lipase polypeptide encoded by a polynucleotide of claim 1.
5. A method for producing a lysosomal acid lipase polypeptide, wherein the method comprises the following steps:
  - 10 a) culturing the host cell of claim 3 under conditions suitable for the expression of the lysosomal acid lipase polypeptide; and
  - b) recovering the lysosomal acid lipase polypeptide from the host cell culture.
- 15 6. A method for detection of a polynucleotide encoding a lysosomal acid lipase polypeptide in a biological sample comprising the following steps:
  - 20 a) hybridizing any polynucleotide of claim 1 to a nucleic acid material of a biological sample, thereby forming a hybridization complex; and
  - b) detecting said hybridization complex.
7. The method of claim 6, wherein before hybridization, the nucleic acid material of the biological sample is amplified.
8. A method for the detection of a polynucleotide of claim 1 or a lysosomal acid lipase polypeptide of claim 4 comprising the steps of:  
contacting a biological sample with a reagent which specifically interacts with  
the polynucleotide or the lysosomal acid lipase polypeptide.

9. A diagnostic kit for conducting the method of any one of claims 6 to 8.
10. A method of screening for agents which decrease the activity of a lysosomal acid lipase, comprising the steps of:
- 5 contacting a test compound with any lysosomal acid lipase polypeptide encoded by any polynucleotide of claim 1;
- detecting binding of the test compound to the lysosomal acid lipase polypeptide, wherein a test compound which binds to the polypeptide is identified as a potential therapeutic agent for decreasing the activity of a
- 10 lysosomal acid lipase.
11. A method of screening for agents which regulate the activity of a lysosomal acid lipase, comprising the steps of:
- 15 contacting a test compound with a lysosomal acid lipase polypeptide encoded by any polynucleotide of claim 1; and
- detecting a lysosomal acid lipase activity of the polypeptide, wherein a test compound which increases the lysosomal acid lipase activity is identified as a potential therapeutic agent for increasing the activity of the lysosomal acid lipase, and wherein a test compound which decreases the lysosomal acid
- 20 lipase activity of the polypeptide is identified as a potential therapeutic agent for decreasing the activity of the lysosomal acid lipase.
12. A method of screening for agents which decrease the activity of a lysosomal acid lipase, comprising the steps of:
- 25 contacting a test compound with any polynucleotide of claim 1 and detecting binding of the test compound to the polynucleotide, wherein a test compound which binds to the polynucleotide is identified as a potential therapeutic agent for decreasing the activity of lysosomal acid lipase.
- 30 13. A method of reducing the activity of lysosomal acid lipase, comprising the steps of:

- 95 -

contacting a cell with a reagent which specifically binds to any polynucleotide of claim 1 or any lysosomal acid lipase polypeptide of claim 4, whereby the activity of lysosomal acid lipase is reduced.

- 5      14. A reagent that modulates the activity of a lysosomal acid lipase polypeptide or a polynucleotide wherein said reagent is identified by the method of any of the claim 10 to 12.
- 10      15. A pharmaceutical composition, comprising:  
the expression vector of claim 2 or the reagent of claim 14 and a pharmaceutically acceptable carrier.
- 15      16. Use of the expression vector of claim 2 or the reagent of claim 14 for the preparation of a medicament for modulating the activity of a lysosomal acid lipase in a disease.
17. Use of claim 16 wherein the disease is cancer, a CNS disorder, obesity, COPD, diabetes, or a cardiovascular disorder.
- 20      18. A cDNA encoding a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6.
19. The cDNA of claim 18 which comprises SEQ ID NO:1, 4 or 7.
- 25      20. The cDNA of claim 18 which consists of SEQ ID NO:1, 4 or 7.
21. An expression vector comprising a polynucleotide which encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6.



- 96 -

22. The expression vector of claim 21 wherein the polynucleotide consists of SEQ ID NO:1, 4 or 7.
- 5 23. A host cell comprising an expression vector which encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6.
24. The host cell of claim 23 wherein the polynucleotide consists of SEQ ID NO:1, 4 or 7.
- 10 25. A purified polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6.
26. The purified polypeptide of claim 25 which consists of the amino acid sequence shown in SEQ ID NO:2, 5 or 6.
- 15 27. A fusion protein comprising a polypeptide having the amino acid sequence shown in SEQ ID NO:2, 5 or 6.
28. A method of producing a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6 comprising the steps of:  
20 culturing a host cell comprising an expression vector which encodes the polypeptide under conditions whereby the polypeptide is expressed; and isolating the polypeptide.
- 25 29. The method of claim 28 wherein the expression vector comprises SEQ ID NO:1, 4 or 7.
30. A method of detecting a coding sequence for a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, comprising the steps of:

hybridizing a polynucleotide comprising 11 contiguous nucleotides of SEQ ID NO:1, 4 or 7 to nucleic acid material of a biological sample, thereby forming a hybridization complex; and detecting the hybridization complex.

- 5      31. The method of claim 30 further comprising the step of amplifying the nucleic acid material before the step of hybridizing.
32. A kit for detecting a coding sequence for a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6, comprising:  
10      a polynucleotide comprising 11 contiguous nucleotides of SEQ ID NO:1, 4 or 7; and  
instructions for the method of claim 30.
33. A method of detecting a polypeptide comprising the amino acid sequence  
15      shown in SEQ ID NO:2, 5 or 6, comprising the steps of:  
contacting a biological sample with a reagent that specifically binds to the polypeptide to form a reagent-polypeptide complex; and  
detecting the reagent-polypeptide complex.
- 20      34. The method of claim 33 wherein the reagent is an antibody.
35. A kit for detecting a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6, comprising:  
an antibody which specifically binds to the polypeptide; and  
25      instructions for the method of claim 33.
36. A method of screening for agents which can modulate the activity of a human lysosomal acid lipase, comprising the steps of:  
contacting a test compound with a polypeptide comprising an amino acid  
30      sequence selected from the group consisting of: (1) amino acid sequences which are at least about 54% identical to the amino acid sequence shown in

SEQ ID NO:2, 5 or 6 and (2) the amino acid sequence shown in SEQ ID NO:2, 5 or 6; and

detecting binding of the test compound to the polypeptide, wherein a test compound which binds to the polypeptide is identified as a potential agent for regulating activity of the human lysosomal acid lipase.

5

37. The method of claim 36 wherein the step of contacting is in a cell.

38. The method of claim 36 wherein the cell is *in vitro*.

10

39. The method of claim 36 wherein the step of contacting is in a cell-free system.

40. The method of claim 36 wherein the polypeptide comprises a detectable label.

15

41. The method of claim 36 wherein the test compound comprises a detectable label.

42. The method of claim 36 wherein the test compound displaces a labeled ligand which is bound to the polypeptide.

20

43. The method of claim 36 wherein the polypeptide is bound to a solid support.

44. The method of claim 36 wherein the test compound is bound to a solid support.

25

45. A method of screening for agents which modulate an activity of a human lysosomal acid lipase, comprising the steps of:

contacting a test compound with a polypeptide comprising an amino acid sequence selected from the group consisting of: (1) amino acid sequences which are at least about 54% identical to the amino acid sequence shown in

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- 99 -

SEQ ID NO:2, 5 or 6 and (2) the amino acid sequence shown in SEQ ID NO:2, 5 or 6; and

detecting an activity of the polypeptide, wherein a test compound which increases the activity of the polypeptide is identified as a potential agent for increasing the activity of the human lysosomal acid lipase, and wherein a test compound which decreases the activity of the polypeptide is identified as a potential agent for decreasing the activity of the human lysosomal acid lipase.

46. The method of claim 45 wherein the step of contacting is in a cell.

47. The method of claim 45 wherein the cell is *in vitro*.

48. The method of claim 45 wherein the step of contacting is in a cell-free system.

49. A method of screening for agents which modulate an activity of a human lysosomal acid lipase, comprising the steps of:

contacting a test compound with a product encoded by a polynucleotide which comprises the nucleotide sequence shown in SEQ ID NO:1, 4 or 7; and detecting binding of the test compound to the product, wherein a test compound which binds to the product is identified as a potential agent for regulating the activity of the human lysosomal acid lipase.

50. The method of claim 49 wherein the product is a polypeptide.

51. The method of claim 49 wherein the product is RNA.

52. A method of reducing activity of a human lysosomal acid lipase, comprising the step of:

contacting a cell with a reagent which specifically binds to a product encoded by a polynucleotide comprising the nucleotide sequence shown in SEQ ID

- 100 -

NO:1, 4 or 7, whereby the activity of a human lysosomal acid lipase is reduced.

- 5
53. The method of claim 52 wherein the product is a polypeptide.
54. The method of claim 53 wherein the reagent is an antibody.
55. The method of claim 52 wherein the product is RNA.
- 10 56. The method of claim 55 wherein the reagent is an antisense oligonucleotide.
57. The method of claim 56 wherein the reagent is a ribozyme.
58. The method of claim 52 wherein the cell is *in vitro*.
- 15 59. The method of claim 52 wherein the cell is *in vivo*.
60. A pharmaceutical composition, comprising:  
a reagent which specifically binds to a polypeptide comprising the amino acid  
20 sequence shown in SEQ ID NO:2, 5 or 6; and  
a pharmaceutically acceptable carrier.
61. The pharmaceutical composition of claim 60 wherein the reagent is an antibody.
- 25 62. A pharmaceutical composition, comprising:  
a reagent which specifically binds to a product of a polynucleotide  
comprising the nucleotide sequence shown in SEQ ID NO:1, 4 or 7; and  
a pharmaceutically acceptable carrier.
- 30

63. The pharmaceutical composition of claim 62 wherein the reagent is a ribozyme.
- 5 64. The pharmaceutical composition of claim 62 wherein the reagent is an antisense oligonucleotide.
65. The pharmaceutical composition of claim 62 wherein the reagent is an antibody.
- 10 66. A pharmaceutical composition, comprising:  
an expression vector encoding a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, 5 or 6; and  
a pharmaceutically acceptable carrier.
- 15 67. The pharmaceutical composition of claim 66 wherein the expression vector comprises SEQ ID NO:1, 4 or 7.
- 20 68. A method of treating a lysosomal acid lipase dysfunction related disease, wherein the disease is selected from cancer, a CNS disorder, obesity, COPD, diabetes, or a cardiovascular disorder comprising the step of:  
administering to a patient in need thereof a therapeutically effective dose of a reagent that modulates a function of a human lysosomal acid lipase, whereby symptoms of the lysosomal acid lipase dysfunction related disease are ameliorated.
- 25 69. The method of claim 68 wherein the reagent is identified by the method of claim 36.
- 30 70. The method of claim 68 wherein the reagent is identified by the method of claim 45.

- 102 -

71. The method of claim 68 wherein the reagent is identified by the method of claim 49.

- 1/13 -

Fig. 1

```
agcttatgac tgggggaaatg acgctgataa tatgaaacat
tacaatcaga gtcaccccc tatatatgac ctgactgcca
tgaaagtgcc tactgctatt tgggctggtg gacatgatgt
cctcgtaca ccccgaggatg tggccaggat actccctcaa
atcaagagtc ttcattactt taagctattg ccagattgga
accactttga ttttgtctgg ggctcgtatg cccctcaacg
gatgtacagt gaaatcatag ctttaatgaa ggcataattcc taa
```

Fig. 2

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AYDWGNDADN MKHYNQSHPP IYDLTAMKVP TAIWAGGHDV
LVTPQDVARI LPQIKSLHYF KLLPDWNHFD FVWGLDAPQR
MYSEIIALMK AYS
```

Fig. 3

```
MKMRFLGLVV CLVLWPLHSE GSGGKLTAVD PETNMNVSEI
ISYWGFPSEE YLVETEDGYI LCLNRIPHGR KNHSDKGPKP
VVFLQHGLLA DSSNWVTNLA NSSLGFIAD AGFDVWMGNS
RGNTWSRKHK TLSVSQDEFW AFSYDEMAKY DLPASINFIL
NKTGQEQVYY VGHSQGTITG FIAFSQIPEL AKRIKMFFAL
GPVASVAFCT SPMAKLGRLP DHLIKDLFGD KEFLPQSAFL
KWLGTHVCTH VILKELCGNL CFLLCGFNER NLNMSRVDVY
TTHSPAGTSV QNMLHWSQAV KFQKFQAFDW GSSAKNYFHY
NQSYPTYNV KDMLVPTAVW SGGHDWLADV YDVNILLTQI
TNLVFHESIP EWEHLDFIWG LDAPWRLYNK IINLMRKYQ
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- 2/13 -

Fig. 4

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atgaaggatt ccgtcaaact gggtatthttg catcatgtag
accactattht cccaacctgc aagtgcata tggcctthtg
cattthctatg atgtggctgc ththtaacaac aacttgthttg
atctgtggaa cththaaatgc tgggtggattc cttgattthtg
aaaatgaagt gaatcctgag gtgtggatga atactagtga
aatcatcatc tacaatggct accccagtga agagtatgaa
gtcaccactg aagatgggta tatactcctt gtcaacagaa
thccttatgg gcgaacacat gctaggagca caggthccccg
gccagthtg tathatgcagc atgcccctgtt tgcagacaa
gcctactggc thgagaatta tgctaathga agcctthgat
thcctthtagc agatgcagggt tatgatgtat ggatgggaaa
cagthcgggga aacactthgggt caagaagaca caaaacactc
tcagagacag atgagaaatt ctgggccttht agthththgatg
aatggccaa atathgatctc ccaggagtaa tagactthcat
tgtaaaataaa actggthcagg agaaathgta ththcattgga
cattcactthg gcactacaa atgggththgta gcctththcca
ccatgcctga actggcacaa agaathcaaaa tgaathththgc
ctthgggtcct acgatctcat thcaaatatcc cacgggcatt
ththaccagggt thththctact thccaaaththc ataathcaagg
ctgththththgg taccaaagggt thctthththtag aagataagaa
aacgaagata gctthctacca aaathctgcaa caathagata
ctctggthtga tatgtagcga atthththgtcc thththggctg
gatccaacaa gaaaaathatg aathcagagthc gaathggatgt
gtathatgtca catgththccca ctggththcatc agthacacaa
athctgcata thaaaacagct ththaccactct gatgaaththca
gagctthatga ctgggggaaat gagctgata aththgaaaca
ththacaaatcag agthcatcccc ctaththththga cctgactgcc
atgaaagthgc ctactgctat ththgggtgggt ggacathgatg
thctcgtaac accccaggat gtggccagga ththctcctca
aatcaagagth ctthcaththct ththagctath gcccagaththgg
aaccactthtg atthththgtctg gggcctcgat gcccctcaac
ggatgtacag tgaaathcata gctthththththga aggcathththc ctaa
```

- 3/13 -

Fig. 5

MKDSVKLVIL HHVDHYFPTC KCIMAFGISM MWLLLTTCCL  
ICGTLNAGGF LDLENEVNPE VWMNTSEIII YNGYPSEEEYE  
VTTEDGYILL VNRIPYGRTH ARSTGPRPVV YMQHALFADN  
AYWLENYANG SLGFLLADAG YDVWMGNSRG NTWSRRHCTL  
SETDEKFWAF SFDEMAKYDL PGVIDFIVNK TGQEKLYFIG  
HSLGTTIGFV AFSTMPELAQ RIKMNFALGP TISFKYPTGI  
FTRFFLLPNS IIKAVFGTKG FFLEDKTKI ASTKICNNKI  
LWLICSEFMS LWAGSNKKNM NQSRMDVYMS HAPTGSSVHN  
ILHIKQLYHS DEFRAWDGN DADNMKHYNQ SHPPIYDLTA  
MKVPTAIWAG GHDVLVTPQD VARILPQIKS LHYFKLLPDW  
NHFDVFWGLD APQRMYSII ALMKAYS

Fig. 6

MKDSVKLVILHHVDHYFPTCKCIMAFGISMWLLLTTCCLICGTLNAGGFLLDL  
ENEVNPEVWMNTSEIIIIYNGYPSEEEYEVTTEDGYILLVNRIPYGRTHARSTGP  
RPVVYMQHALFADNAYWLENYANGSLGFLLADAGYDVWMGNSRGNTWSRRHKT  
LSETDEKFWAFRYTKGCNATAERAKQMEMPGPYWAIVDARES PFLFGNREESR  
GLKNTQAYDWGNDADNMKHYNQSHPPIYDLTAMKVPTAIWAGGHDVLVTPQDV  
ARILPQIKSLHYFKLLPDWNHFDVFWGLDAPQRMYSIIALMKAYS

- 4/13 -

Fig. 7

Atgaaggattccgtcaaactgggttattttgcatcatgtagaccactattttccc  
aacctgcaagtgcacatcatggccttttggcattttctatgatgtggctgcttttaa  
caacaacttggttgatctgtggaactttaaatgctgggtggattccttgatttg  
gaaaatgaagtgaatcctgaggtgtggatgaatactagtgaatcatcatcta  
caatggctaccccagtgagagtatgaagtcaccactgaagatgggtatatac  
tccttggtcaacagaattccttatgggcgaacacatgctaggagcacaggtccc  
cggccagttgtgtatatgcagcatgccctggttgcagacaatgcctactggct  
tgagaattatgctaattggaagccttggattccttctagcagatgcaggttatg  
atgtatggatgggaaacagtcggggaaacacttgggtcaagaagacacaaaaca  
ctctcagagacagatgagaaattctgggccttttagatatataaaaggggtgcaa  
tgctactgctgaaagagcaaagcaaattggagatgcctgggtccttactgggcca  
tcgtggatgctagggaaagccccctttctttttggaaacaggggaagagtctaga  
gggttgaaaaacacccaagcttatgactggggaaatgacgctgataatatgaa  
acattacaatcagagtcacccccctatatatgacctgactgccatgaaagtgc  
ctactgctattttgggctgggtggacatgatgtcctcgtaacaccccaggatgtg  
gccaggatactccctcaaatacaagagtcctcattactttaagctattgccaga  
ttggaaccactttgatTTTTGTCTGGGGCCTCGATGCCCTCAACGGATGTACA  
GTGAAATCATAGCTTTAATGAAGGCATATTCCTAA

- 5/13 -

Fig. 8

BLASTP - alignment of 135\_PROTEIN against swiss|P38571|LICH\_HUMAN  
 This hit is scoring at : 4e-26 (expectation value)  
 Alignment length (overlap) : 92  
 Identities : 53 %  
 Scoring matrix : BLOSUM62 (used to infer consensus pattern)  
 Database searched : nrdb

Q: 1 AYDWGNDADNMKHYNQSHPIYDLTAMKVPTAIWAGHDVLVTPQDVARIIPQIKSLHYF  
 A:DWG:.A.N. HYNQS:PP.Y:.. M VPTA:W:GGHD L.. .DV :L.QI.:L :.  
 H: 307 AFDWGSSAKNYFHYNQSYPTYNVVKDMLVPTAVWSGGHDWLADVYDVNILLTQITNLVVFH

KLDPDWNHFDVFWGLDAPQRMYSIIALMKAY 92  
 : :P:W.H.DF:WGLDAP R:Y::II LM:.Y  
 ESIPEWEHLDFIWWGLDAPWRRLYNKIINLMRKY 398

- 6/13 -

Fig. 9

BLASTP - alignment of 135\_PROTEIN against pdb|1HLG|1HLG-A  
 lipase, gastric  
 This hit is scoring at : 1e-25 (expectation value)  
 Alignment length (overlap) : 89  
 Identities : 50 %  
 Scoring matrix : BLOSUM62 (used to infer consensus pattern)  
 Database searched : nrdb  
 Q: 1 AYDWGNDADNMKHYNQSHPPYDILTAMKVPTAIWAGHDVLTVPQDVARILPQIKSLHYF  
 AYDWG:...N..HY:QS.PP.Y::TAM.VP.A:W GG.D:L..PQDV. :LP:::L Y.  
 H: 275 AYDWGSPVQNRMHYDQSOPPYNVVTAMNVPPIAVWNGGKDLLADPQDVGLLLPKLPNLIYH  
 KLLPDWNHFDFFVWGLDAPQRMYSIIALM 89  
 K : P : NH.DF:W.:DAPQ.:Y::I:::  
 KEIPFYNHLDFTIWAMDAPQEVYNDIVSMI 363

- 7/13 -

Fig. 10

BLASTP - alignment of 135\_v2\_TR1 against swiss|P38571|LICH\_HUMAN

This hit is scoring at : 5e-125 (expectation value)

Alignment length (overlap) : 396

Identities : 53 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 31 MWLLLTTCITLNCAGGFLDLENEVNPVMMNTSEIIYNGYPSEYEVTTEDGYILL

M .L . . . . CL: . . L: . . G . . . V:PE. MN.SEII Y G:PSEY V.TEDGYIL.

H: 3 MRFLGLVVCLVPLHSEGGGKLTAVDPETNMNVSEIIISYWGFPSEYLVETEDGYILC

VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVMMGNSRG

:NRIP:GR: . . . GP:PVV::QH.L.AD:: W:N.AN.SLGF:LADAG:DVMMGNSRG

LNRI PHGRKNHSDKGPKPVVFLQHGLLADSSNWVTNLANSLSGLFILLADAGFDVMMGNSRG

NTWSRRHKTLSETDEKFWAFSDEMAYDLPGVIDFIVNKTQEKLYFIGHSLGTTIGFV

NTWSR:HKTL: . . :FWAFS:DEMAYDLP. I:FI:NKTQE::Y::GHS GTTIGF:

NTWSRHKTLVSQDEFWAFSDEMAYDLPASINFILNKTQEQVYVVGHSQGTTIGFI

LIPASE\_SER region [prosite]

S is the active site charge relay system

AFSTMPELAQRKMNFAFGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKI

AFS.:PELA:RIKM FALGP..S.: T. . . . LP:::IK :FG.K F. :...K

AFSQIPELAKRIKMFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKFELPQSAFLKW

ASTKICNNKILWLICSEFMSLWAGSNKKMNQSRMDVYMSHAPTGSVVHNLHIKQLYHS

.T.:C.: IL :C.... L .G N::N:N.SR:DVY.:H:P.G:SV.N:LH .Q...

LGTHVCTHVILKELCGNLCFLLCGFNERNLMSRVDVYTTTHSPAGTSVQNMLHWSQAVKF

- 8/13 -

Fig. 10 (continued)

```

DEFRA YD W G N D A D N M K H Y N Q S H P P I Y D L T A M K V P T A I W A G H D V L V T P Q D V A R I L P Q I K S
.: F : A : D W G : . A . N . H Y N Q S : P P . Y : . . M V P T A : W : G G H D L . . . D V : L . Q I . :
Q K F Q A F D W G S S A K N Y F H Y N Q S Y P P T Y N V K D M L V P T A V W S G G H D W L A D V Y D V N I L L T Q I T N

L H Y F K L L P D W N H F D F V W G L D A P Q R M Y S E I I A L M K A Y 426
L : . . : P : W . H . D F : W G L D A P R : Y : . I I L M : . Y
L V F H E S I P E W E H L D F I N G L D A P W R L Y N K I I N L M R K Y 398

```

ACT SITE charge relay system

3D structure inferred by clear homology from residues 58 to 423 in 1HLG-A

- 9/13 -

BLASTP - alignment of 135\_v2\_TR1 against pdb|1HLG|1HLG-A; lipase, gastric  
This hit is scoring at : 5e-117 (expectation value)

Alignment length (overlap) : 366

Identities : 52 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 58 NPEVMMNTSEIIYNGYPSEEEYEVTTEDGYILLVNRIPIYGRTHARSTGPRPVVYMQHALF

:PEV MN.S::I.Y GYP:EEYEV.TEDGYIL VNRIPYG: ::G.RPVV::QH.L.

H: 1 SPEVTMNISQMITYWGYPNEEYEVVTTEDGYILEVNRIPYK---KN\$QQRPVVFLQHGLL

ADNAYWLENYANGSLGFLILADAGYDVMMGNSRGNTWSRRHKTLSLSEDEKFWAFSFDDEMAK

A. . W:.N..N.SL.F:LADAGYDVW:GNSRGNTW:RR: .S... :FWAFSFDDEMAK

ASATNWSNLPNNSLAFILADAGYDVWLGNSRGNTWARRNLIYSPDSVEFWAFSFDDEMAK

YDLPGVIDFIVNKTQEKLYFIGHSLGTTIGFVAFSTMPPELAQRIKMNFAALGPTISFKYP

YDLP..IDFIV.KTGQ::L::GHS GTTIGF:AFST P.LA:RIK. :AL.P...:KY.

YDLPATIDFIVKKTGQKQLHYVGH\$QGTIGFIAFSTNPSLAKRIKTFYALAPVATVKYT

TGIFTRFFELLPNSIIKAVFGTKGFFLEDKTKIASTKICNNKILWLICSEFMSLWAGSNK

.....:P.S:.K :FG.K F: : :...:T::C:::L L:CS. : : .G : :

KSLINKLRFVPQSLFKFIFGDKIFYPHNFDDQFLATEVCSREMLNLLCSNALFIICGFDS

KNMNQSRMDVYMSHAPTGS\$VHNILHIKQLYHSDEFRAVDWGNADNMKHYNQSHPPIYD

KN.N.SR:DVI:SH P.G:SV.N:.H .Q...S:.F:AYDWG:...N..HY:QS.PP.Y:

KNFNTSRLLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYIN

LTAMKVPTAIWAGGHDVLTVPQDVARILPQIKSLHYFKLLPDWNHFD\$VWGLDAPQRMYS

:TAM.VP.A:W GG.D:L..PQDV. :LP:::L Y.K :P :NH.DF:W.:DAPQ.:Y:

VTAMNVP\$IAVWNGGKDLLADPQDVGLLLPKLPNLIYHKEIPFYNHLDFTWAMDAPQEVYN

EIIALM 423

:I:::

DIVSMI 363



- 10/13 -

Fig. 12

Exon/intron junctions for 135\_v2 (1st and 2nd exons from genscan, the rest derived by genewise, and the last exon extended to stop according to genscan):  
Q = 135\_v2; H = AL358532.9 on REVERSE complement strand

```

exon 1
Q:      1 atgaaggattccgtcaaaactgggtattttgcatcatgtagaccactatttcccaacctgc
H: 47381 atgaaggattccgtcaaaactgggtattttgcatcatgtagaccactatttcccaacctgc
      aagtgcacatggcctttg      79
      aagtgcacatggcctttg(gtgtg... 47303

exon 2
Q:      80 gcatttctatgatgtggctgcttttaacaacaaacttgtttgatctgtggaacttttaaat
H: 45813 ..cag)gcatttctatgatgtggctgcttttaacaacaaacttgtttgatctgtggaacttttaaat
      gctgggtgattcccttgatttggaaaaatgaagtgaatcctgaggtgtggatgaatact      195
      gctgggtgattcccttgatttggaaaaatgaagtgaatcctgaggtgtggatgaatact(gttaa... 45698

exon 3
Q:      196 agtgaaaatcatcatctacaaatggctacccagtggaagagtatgaagtcaccactgaagat
H: 45023 ..cag)agtgaaaatcatcatctacaaatggctacccagtggaagagtatgaagtcaccactgaagat
      gggatataactccttgtcaacagaaattccttatggcgaaacacatgctaggagcacag      313
      gggatataactccttgtcaacagaaattccttatggcgaaacacatgctaggagcacag(gtac... 44906

exon 4
Q:      313 gtccccggccagttgtgtatatgcagcatgccctgtttgcagacaatgcctactggc
H: 42801 ..ccag)gtccccggccagttgtgtatatgcagcatgccctgtttgcagacaatgcctactggc
      atgagaaaattctgggccttttag      512
      atgagaaaattctgggccttttag(gttaa... 42603

exon 5
Q:      513 tttttgatgaaatggccaaaatatgatctcccaggagtaataagacttcatgttaataaaa
H: 40942 ..gcag)tttttgatgaaatggccaaaatatgatctcccaggagtaataagacttcatgttaataaaa

```

- 11/13 -

Fig. 12 (continued)

actggtcaggagaaattgtatttcatcaggacattcacttggcactacaatag 622  
 actggtcaggagaaattgtatttcatcaggacattcacttggcactacaatag (gtat... 40833

exon 6  
 Q: 623  
 H: 38419      ggtttgtagcctttccaccatgcctgaactggcacaaagaatcaaaatgaatttttgc  
 ...tcag) ggtttgtagcctttccaccatgcctgaactggcacaaagaatcaaaatgaatttttgc  
 tccaaatccataatcaag 759  
 tccaaatccataatcaag (gtag... 38283

exon 7  
 Q: 760  
 H: 36366      gctgtttttggtaccaaaagggtttctttttagaagataagaaaacgaagatagcttcta  
 ...atag) gctgtttttggtaccaaaagggtttctttttagaagataagaaaacgaagatagcttcta  
 ctggatccaacaagaaaatatgaatcag 906  
 ctggatccaacaagaaaatatgaatcag (gtat... 36220

exon 8  
 Q: 907  
 H: 32738      agtcgaatggatgtgtatatgtgcacatgctcccactggttcatcagtacacacaacattc  
 ...ttag) agtcgaatggatgtgtatatgtgcacatgctcccactggttcatcagtacacacaacattc  
 tgcataataaaacag 978  
 tgcataataaaacag (gtag... 32667

exon 9  
 Q: 979  
 H: 32119      ctttaccactctgatgaattcagagcttatgactggggaatgacgctgataaatatg  
 ...tcag) ctttaccactctgatgaattcagagcttatgactggggaatgacgctgataaatatg  
 aacattacaatcag 1050  
 aacattacaatcag (gtga... 32048

exon 10  
 Q: 1051  
 H: 29202      agtcacccccctatatatgacctgactgccatgaaagtgcctactgctatttgggct  
 ...acag) agtcacccccctatatatgacctgactgccatgaaagtgcctactgctatttgggct  
 gatgccccctcaacggatgtacagtgaatcatagctttaatgaaggcatattcctaa 1284  
 gatgccccctcaacggatgtacagtgaatcatagctttaatgaaggcatattcctaa 28969

- 12/13 -

Fig. 13

## Exon-intron structure:

gi 11414589 emb AL358532.9 AL358532	GeneWise	gi 585405 sp P38571 LICH_HUMAN
match 28973 45023		
cds 45022 44904	intron 44905 42802	
cds 42800 42601	intron 42602 40943	
cds 40941 40831	intron 40832 38420	
cds 38418 38281	intron 38282 36367	
cds 36365 36218	intron 36219 32739	
cds 32737 32665	intron 32666 32120	
cds 32118 32046	intron 32047 29203	
cds 29201 28973		

- 13/13 -

Fig. 13

Genscan output relevant protion:

Gn.Ex	Type	S	.Begin	...End	.Len	Fr	Ph	I/Ac	Do/T	CodRg	P.....	Tscr..	in	in	genewise?
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----
2.08	PlyA	-	25957	25952	6		0	129	36	167	0.983	1.05			Y
2.07	Term	-	29202	28969	234	0	1	22	99	66	0.089	10.94			n
2.06	Intr	-	32096	32048	49	1	1	82	63	90	0.230	-1.14			n
2.05	Intr	-	39053	38913	141	1	0					4.45			n
2.04	Intr	-	42801	42603	199	1	1	128	67	176	0.901	16.99			Y
2.03	Intr	-	45023	44906	118	2	1	59	87	137	0.957	9.82			Y
2.02	Intr	-	45813	45698	116	1	2	42	93	66	0.826	1.75			n
2.01	Init	-	47381	47303	79	2	1	97	62	55	0.808	5.07			n
2.00	Prom	-	51042	51003	40							-6.45			

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## SEQUENCE LISTING

&lt;110&gt; Bayer AG

&lt;120&gt; HUMAN LYSOSOMAL ACID LIPASE

&lt;130&gt; LIO200 Foreign Countries

&lt;150&gt; US 60/244,215

&lt;151&gt; 2000-10-31

&lt;150&gt; US 60/251,401

&lt;151&gt; 2000-12-06

&lt;160&gt; 7

&lt;170&gt; PatentIn version 3.1

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283

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Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn Gln  
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Ser His Pro Pro Ile Tyr Asp Leu Thr Ala Met Lys Val Pro Thr Ala  
20 25 30

Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val Ala  
35 40 45

Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu Pro  
50 55 60

Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln Arg  
65 70 75 80

Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser  
85 90

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Leu His Ser Glu Gly Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu  
20 25 30

- 3 -

Thr Asn Met Asn Val Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser  
 35 40 45

Glu Glu Tyr Leu Val Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn  
 50 55 60

Arg Ile Pro His Gly Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro  
 65 70 75 80

Val Val Phe Leu Gln His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val  
 85 90 95

Thr Asn Leu Ala Asn Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly  
 100 105 110

Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys  
 115 120 125

His Lys Thr Leu Ser Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr  
 130 135 140

Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu  
 145 150 155 160

Asn Lys Thr Gly Gln Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly  
 165 170 175

Thr Thr Ile Gly Phe Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys  
 180 185 190

Arg Ile Lys Met Phe Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe  
 195 200 205

Cys Thr Ser Pro Met Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile  
 210 215 220

Lys Asp Leu Phe Gly Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu  
 225 230 235 240

Lys Trp Leu Gly Thr His Val Cys Thr His Val Ile Leu Lys Glu Leu  
 245 250 255

Cys Gly Asn Leu Cys Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu  
 260 265 270

- 4 -

Asn Met Ser Arg Val Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr  
 275 280 285

Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys  
 290 295 300

Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr  
 305 310 315 320

Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro  
 325 330 335

Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp  
 340 345 350

Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser  
 355 360 365

Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro  
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 180

gtgtggatga atactagtga aatcatcatc tacaatggct accccagtga agagtatgaa  
 240

gtcaccactg aagatgggta tatactcctt gtcaacagaa ttccttatgg gcgaacacat  
 300

gctaggagca caggccccg gccagttgtg tatatgcagc atgccctggt tgcagacaat  
 360



- 5 -

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660

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720

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1080

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1140

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Phe Pro Thr Cys Lys Cys Ile Met Ala Phe Gly Ile Ser Met Met Trp  
 20 25 30

Leu Leu Leu Thr Thr Thr Cys Leu Ile Cys Gly Thr Leu Asn Ala Gly  
 35 40 45

Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val Trp Met Asn  
 50 55 60

Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu Glu Tyr Glu  
 65 70 75 80

Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg Ile Pro Tyr  
 85 90 95

Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val Val Tyr Met  
 100 105 110

Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu Asn Tyr Ala  
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Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr Asp Val Trp  
 130 135 140

Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His Lys Thr Leu  
 145 150 155 160

Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp Glu Met Ala  
 165 170 175

Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn Lys Thr Gly  
 180 185 190

Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr Thr Ile Gly  
 195 200 205

Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg Ile Lys Met  
 210 215 220

Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro Thr Gly Ile  
 225 230 235 240

- 7 -

Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys Ala Val Phe  
 245 250 255

Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys Ile Ala Ser  
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Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys Ser Glu Phe  
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 305 310 315 320

Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe Arg Ala Tyr  
 325 330 335

Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn Gln Ser His  
 340 345 350

Pro Pro Ile Tyr Asp Leu Thr Ala Met Lys Val Pro Thr Ala Ile Trp  
 355 360 365

Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val Ala Arg Ile  
 370 375 380

Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu Pro Asp Trp  
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Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln Arg Met Tyr  
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Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser  
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<213> Homo sapiens

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 20 25 30  
 Leu Leu Leu Thr Thr Thr Cys Leu Ile Cys Gly Thr Leu Asn Ala Gly  
 35 40 45  
 Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val Trp Met Asn  
 50 55 60  
 Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu Glu Tyr Glu  
 65 70 75 80  
 Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg Ile Pro Tyr  
 85 90 95  
 Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val Val Tyr Met  
 100 105 110  
 Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu Asn Tyr Ala  
 115 120 125  
 Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr Asp Val Trp  
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 Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His Lys Thr Leu  
 145 150 155 160  
 Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Arg Tyr Thr Lys Gly Cys  
 165 170 175  
 Asn Ala Thr Ala Glu Arg Ala Lys Gln Met Glu Met Pro Gly Pro Tyr  
 180 185 190  
 Trp Ala Ile Val Asp Ala Arg Glu Ser Pro Phe Leu Phe Gly Asn Arg  
 195 200 205  
 Glu Glu Ser Arg Gly Leu Lys Asn Thr Gln Ala Tyr Asp Trp Gly Asn  
 210 215 220  
 Asp Ala Asp Asn Met Lys His Tyr Asn Gln Ser His Pro Pro Ile Tyr  
 225 230 235 240

- 9 -

Asp Leu Thr Ala Met Lys Val Pro Thr Ala Ile Trp Ala Gly Gly His  
                                   245                                  250                                  255

Asp Val Leu Val Thr Pro Gln Asp Val Ala Arg Ile Leu Pro Gln Ile  
                                   260                                  265                                  270

Lys Ser Leu His Tyr Phe Lys Leu Leu Pro Asp Trp Asn His Phe Asp  
                                   275                                  280                                  285

Phe Val Trp Gly Leu Asp Ala Pro Gln Arg Met Tyr Ser Glu Ile Ile  
                                   290                                  295                                  300

Ala Leu Met Lys Ala Tyr Ser  
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- 10 -

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